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OM protein - protein search, using SW model

Run on: February 9, 2004, 11:34:39 ; Search time 28 Seconds
(without alignments)
497.153 Million cell updates/sec

Title: US-10-004-176-6

Sequence: 1 VASAGIGPEVPPDRDFEPL.....QPTFCVYVRSALQGNK 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Issued Patents AA:

- 1: /cgn2_6/prodata/2/1aa/5A_COMB.pep.*
- 2: /cgn2_6/prodata/2/1aa/5B_COMB.pep.*
- 3: /cgn2_6/prodata/2/1aa/6A_COMB.pep.*
- 4: /cgn2_6/prodata/2/1aa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/prodata/2/1aa/backfillseq.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1709	99.8	333	1	US-08-442-063A-27
2	1709	99.8	359	1	US-08-303-238-4
3	1709	99.8	359	3	US-08-458-834-4
4	1704	99.5	342	1	US-08-372-919-2
5	1704	99.5	342	1	US-08-619-916-2
6	1704	99.5	342	5	PCT-US95-08542-2
7	1653	96.5	353	6	5340934-4
8	1567	91.5	307	1	US-08-442-063A-48
9	1433	83.7	282	1	US-08-442-063A-45
10	1186	69.2	236	1	US-08-442-063A-42
11	966	56.4	358	3	US-08-303-238-3
12	966	56.4	358	3	US-08-458-834-3
13	965	56.3	368	6	5340934-2
14	948	54.0	188	1	US-08-442-063A-39
15	925.5	54.0	373	4	US-09-724-864-43
16	714	41.7	141	1	US-08-442-063A-36
17	488	28.5	96	1	US-08-442-063A-33
18	341	19.9	649	3	US-09-188-930-303
19	341	19.9	649	4	US-09-312-283C-305
20	326.5	19.1	376	3	US-08-458-834-1
21	326.5	19.1	376	3	US-08-303-238-1
22	323	18.9	1480	3	US-09-191-647-7
23	323	18.9	1480	3	US-09-540-245A-7
24	323	18.9	1480	3	US-09-540-153-7
25	323	18.9	1480	5	PCT-US91-09055-2
26	321	18.7	1480	4	US-09-182-024A-5
27	321	18.7	1529	4	US-09-312-283C-396

28	320	18.7	1523	4	US-09-182-024A-2	Sequence 2, App1
29	317	18.5	1525	3	US-09-191-647-2	Sequence 2, App1
30	317	18.5	1525	3	US-09-540-245A-2	Sequence 2, App1
31	317	18.5	1525	3	US-09-540-153-2	Sequence 2, App1
32	314.5	18.4	375	1	US-08-303-238-2	Sequence 2, App1
33	314.5	18.4	375	1	US-08-458-834-2	Sequence 2, App1
34	303.5	17.7	653	4	US-09-996-243-229	Sequence 229, App
35	302	17.6	640	4	US-09-996-243-501	Sequence 501, App
36	295.5	17.3	907	4	US-09-170-496D-264	Sequence 264, App
37	295.5	17.3	907	4	US-09-170-496D-278	Sequence 278, App
38	291	17.0	1091	3	US-08-986-485-5	Sequence 5, App1
39	281.5	16.4	302	4	US-09-482-273-105	Sequence 105, App
40	280	16.3	55	1	US-08-442-063A-57	Sequence 57, App1
41	278	16.2	1101	3	US-08-986-485-2	Sequence 2, App1
42	273	15.9	605	1	US-08-190-802A-49	Sequence 49, App1
43	273	15.9	605	3	US-09-063-950-5	Sequence 5, App1
44	273	15.9	605	3	US-08-477-346-49	Sequence 49, App1
45	273	15.9	605	4	US-08-473-089-49	Sequence 49, App1

ALIGNMENTS

RESULT 1
US-08-442-063A-27
; Sequence 27, Application US/08442063A
; Patent No. 5705609
; GENERAL INFORMATION:
; APPLICANT: RUOSLAHTI, ERKKI I.
; APPLICANT: PIERSCHACHER, MICHAEL D.
; APPLICANT: CARDENAS, JOSE
; APPLICANT: CRAIG, WILLIAM
; APPLICANT: MILLER, DANIEL G.
; TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF
; INHIBITING CELL REGULATORY FACTORS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,063A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865,652
; FILING DATE: 03-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHERIN A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1454
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-442-063A-27
Query Match 99.8%; Score 1709; DB 1; Length 333;
Best Local Similarity 100.0%; Pred. No. 4.6e-156;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDDDFEPSLGPVCPFRQCHLRVQCSDGLDKVLPKOLPDDTLLDIQNN 61
DB 4 EASGIGPEVDDDDFEPSLGPVCPFRQCHLRVQCSDGLDKVLPKOLPDDTLLDIQNN 63
QY 62 KITEIKDGPDKNLKHALILVNNKISKVSPGAFPLVKLERLYLSKNOLKEIPKKPKT 121
DB 64 KITEIKDGPDKNLKHALILVNNKISKVSPGAFPLVKLERLYLSKNOLKEIPKKPKT 123
QY 122 LOELRAHENEITVKRVKTFNGLNQMIIVIELGTPNPLKSSGIENGAFOQMKLSYIRIADTN 181
DB 124 LOELRAHENEITVKRVKTFNGLNQMIIVIELGTPNPLKSSGIENGAFOQMKLSYIRIADTN 183
QY 182 ITSIPQGLPPSLTELHLDGKISRVDASIKGINLAKLGLSFNSISAVNGSLANTPHL 241
DB 184 ITSIPQGLPPSLTELHLDGKISRVDASIKGINLAKLGLSFNSISAVNGSLANTPHL 243
QY 242 RELHLDNNKLTFRVGGIAEHKYLQVYVLIHNNNISVVGSSDFCPGHNTKKAASYGVLSFS 301
DB 244 RELHLDNNKLTFRVGGIAEHKYLQVYVLIHNNNISVVGSSDFCPGHNTKKAASYGVLSFS 303
QY 302 NPVOYWEIOPSTFRVCYVRSALQGNKY 329
DB 304 NPVOYWEIOPSTFRVCYVRSALQGNKY 331

RESULT 2
US-08-303-238-4
Sequence 4, Application US/08303238
Patent No. 5654270
GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: LONGAKER, MICHAEL T.
APPLICANT: WHITBY, DAVID J.
APPLICANT: HARPER, JOHN R.
APPLICANT: PIERSCBACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSER: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,238
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: P-LA 9453
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-303-238-4

Query Match 99.8%; Score 1709; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 5,2e-158;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EASGIGPEVDDDDFEPSLGPVCPFRQCHLRVQCSDGLDKVLPKOLPDDTLLDIQNN 61
DB 32 EASGIGPEVDDDDFEPSLGPVCPFRQCHLRVQCSDGLDKVLPKOLPDDTLLDIQNN 91
QY 62 KITEIKDGPDKNLKHALILVNNKISKVSPGAFPLVKLERLYLSKNOLKEIPKKPKT 121
DB 92 KITEIKDGPDKNLKHALILVNNKISKVSPGAFPLVKLERLYLSKNOLKEIPKKPKT 151
QY 122 LOELRAHENEITVKRVKTFNGLNQMIIVIELGTPNPLKSSGIENGAFOQMKLSYIRIADTN 181
DB 152 LOELRAHENEITVKRVKTFNGLNQMIIVIELGTPNPLKSSGIENGAFOQMKLSYIRIADTN 211
QY 182 ITSIPQGLPPSLTELHLDGKISRVDASIKGINLAKLGLSFNSISAVNGSLANTPHL 241
DB 212 ITSIPQGLPPSLTELHLDGKISRVDASIKGINLAKLGLSFNSISAVNGSLANTPHL 271
QY 242 RELHLDNNKLTFRVGGIAEHKYLQVYVLIHNNNISVVGSSDFCPGHNTKKAASYGVLSFS 301
DB 272 RELHLDNNKLTFRVGGIAEHKYLQVYVLIHNNNISVVGSSDFCPGHNTKKAASYGVLSFS 331
QY 302 NPVOYWEIOPSTFRVCYVRSALQGNKY 329
DB 332 NPVOYWEIOPSTFRVCYVRSALQGNKY 359

RESULT 3
US-08-458-834-4
Sequence 4, Application US/08458834
Patent No. 627812
GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: LONGAKER, MICHAEL T.
APPLICANT: WHITBY, DAVID J.
APPLICANT: HARPER, JOHN R.
APPLICANT: PIERSCBACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSER: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,834
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: P-LA 9453
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-834-4

Query Match 99.8%; Score 1709; DB 3; Length 359;
Best Local Similarity 100.0%; Pred. No. 5,2e-158;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDRDPEPSIGVPCPCQCCHLRVVOCSDLGLKVPKDLPPDTLLDLQNN 61
DB 32 EASGIGPEVDDRDPEPSIGVPCPCQCCHLRVVOCSDLGLKVPKDLPPDTLLDLQNN 91
QY 62 KITEIKDGFKNLKNLHALILVNNKISKVSPGAFPLVLERLYSKNOLKELPEKMPKT 121
DB 92 KITEIKDGFKNLKNLHALILVNNKISKVSPGAFPLVLERLYSKNOLKELPEKMPKT 151
QY 122 LOELRAHENEITKRVKVTENGINQMI VIELGTNPLKSSGIEGAFQGMKKLSYIRIADTN 181
DB 152 LOELRAHENEITKRVKVTENGINQMI VIELGTNPLKSSGIEGAFQGMKKLSYIRIADTN 211
QY 182 ITSIPQGLPPSLTEHLHDGNKISRVDASLKGILNIAKGLSPNLSAVDNGSLANTPHL 241
DB 212 ITSIPQGLPPSLTEHLHDGNKISRVDASLKGILNIAKGLSPNLSAVDNGSLANTPHL 271
QY 242 RELHLDNNKLTVPGLAEHKYIQVYLLHNNNISVVGSSDFCPGHNTKKAISGVSLPS 301
DB 272 RELHLDNNKLTVPGLAEHKYIQVYLLHNNNISVVGSSDFCPGHNTKKAISGVSLPS 331
QY 302 NPQYWEIQPSTFRVCYVRSALQLGNYK 329
DB 332 NPQYWEIQPSTFRVCYVRSALQLGNYK 359

RESULT 4

US-08-272-919-2

Sequence 2, Application US/08272919
Patent No. 5567807

GENERAL INFORMATION:

APPLICANT: Craig, William S.
APPLICANT: Harper, John R.
APPLICANT: Hernandez, Sam D.
APPLICANT: Koestel, Paul J.
APPLICANT: Parker, Jonathan R.
APPLICANT: Vedvick, Thomas S.
TITLE OF INVENTION: Processes for the Purification of Human
TITLE OF INVENTION: Recombinant Decorin and the Detection of Guanidinium Ions
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/272,919
FILING DATE: 08-JUL-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 342 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-272-919-2

Query Match 99.5%; Score 1704; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 1,5e-157;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDRDPEPSIGVPCPCQCCHLRVVOCSDLGLKVPKDLPPDTLLDLQNN 61
DB 16 EASGIGPEVDDRDPEPSIGVPCPCQCCHLRVVOCSDLGLKVPKDLPPDTLLDLQNN 75
QY 62 KITEIKDGFKNLKNLHALILVNNKISKVSPGAFPLVLERLYSKNOLKELPEKMPKT 121
DB 76 KITEIKDGFKNLKNLHALILVNNKISKVSPGAFPLVLERLYSKNOLKELPEKMPKT 135
QY 122 LOELRAHENEITKRVKVTENGINQMI VIELGTNPLKSSGIEGAFQGMKKLSYIRIADTN 181
DB 136 LOELRAHENEITKRVKVTENGINQMI VIELGTNPLKSSGIEGAFQGMKKLSYIRIADTN 195
QY 182 ITSIPQGLPPSLTEHLHDGNKISRVDASLKGILNIAKGLSPNLSAVDNGSLANTPHL 241
DB 196 ITSIPQGLPPSLTEHLHDGNKISRVDASLKGILNIAKGLSPNLSAVDNGSLANTPHL 255
QY 242 RELHLDNNKLTVPGLAEHKYIQVYLLHNNNISVVGSSDFCPGHNTKKAISGVSLPS 301
DB 256 RELHLDNNKLTVPGLAEHKYIQVYLLHNNNISVVGSSDFCPGHNTKKAISGVSLPS 315
QY 302 NPQYWEIQPSTFRVCYVRSALQLGNYK 328
DB 316 NPQYWEIQPSTFRVCYVRSALQLGNYK 342

RESULT 5

US-08-619-916-2

Sequence 2, Application US/08619916
Patent No. 5763276

GENERAL INFORMATION:

APPLICANT: Craig, William S.
APPLICANT: Harper, John R.
APPLICANT: Hernandez, Sam D.
APPLICANT: Koestel, Paul J.
APPLICANT: Parker, Jonathan R.
APPLICANT: Vedvick, Thomas S.
TITLE OF INVENTION: Processes for the Purification of Human
TITLE OF INVENTION: Recombinant Decorin and the Detection of Guanidinium Ions
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,916
FILING DATE: 08-JUL-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1040
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-619-916-2

Query Match 99.5%; Score 1704; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.5e-157;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDDDFEPSLGPVCPFCQCHLRVQCSDDLGLDKVPKOLPDDTLLDLONN 61
DB 16 EASGIGPEVDDDDFEPSLGPVCPFCQCHLRVQCSDDLGLDKVPKOLPDDTLLDLONN 75
QY 62 KITEIKDGDPRKLNKNHALILVNNKISKVSPGAFPLVKLERLYLSKNQKELPERKPKT 121
DB 76 KITEIKDGDPRKLNKNHALILVNNKISKVSPGAFPLVKLERLYLSKNQKELPERKPKT 135
QY 122 LOELRAHENEITKVRKVTENGLOMIVIELGTNPLKSSGIENGAFQGMKKLSYIRADTN 181
DB 136 LOELRAHENEITKVRKVTENGLOMIVIELGTNPLKSSGIENGAFQGMKKLSYIRADTN 195
QY 182 ITSIPQGLPSSLTELHLDGKISRVDASLKGANNLAKGLSPNSISAVDNGSLANTPHL 241
DB 196 ITSIPQGLPSSLTELHLDGKISRVDASLKGANNLAKGLSPNSISAVDNGSLANTPHL 255
QY 242 RELHLDNNKLTTRVPGGLAEHKYIQVYVTLHNNNISVVGSSDFCPGHNTKKAASYGVLSFS 301
DB 256 RELHLDNNKLTTRVPGGLAEHKYIQVYVTLHNNNISVVGSSDFCPGHNTKKAASYGVLSFS 315
QY 302 NPVOYWEIOPSTFRVCYVRSALQLGNY 328
DB 316 NPVOYWEIOPSTFRVCYVRSALQLGNY 342

RESULT 6
PCT-US95-08542-2
Sequence 2, Application PC/TUS9508542
GENERAL INFORMATION:
APPLICANT: La Jolla Cancer Research Foundation
TITLE OF INVENTION: Processes for the Purification of Human
TITLE OF INVENTION: Recombinant Decorin and the Detection of Guanidinium
TITLE OF INVENTION: Ions
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08542
FILING DATE: 07-JUL-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Susan M.
REGISTRATION NUMBER: 36,405
REFERENCE/DOCKET NUMBER: FP-LA 1751
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08542-2

Query Match 99.5%; Score 1704; DB 5; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.5e-157;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDDDFEPSLGPVCPFCQCHLRVQCSDDLGLDKVPKOLPDDTLLDLONN 61
DB 16 EASGIGPEVDDDDFEPSLGPVCPFCQCHLRVQCSDDLGLDKVPKOLPDDTLLDLONN 75
QY 62 KITEIKDGDPRKLNKNHALILVNNKISKVSPGAFPLVKLERLYLSKNQKELPERKPKT 121
DB 76 KITEIKDGDPRKLNKNHALILVNNKISKVSPGAFPLVKLERLYLSKNQKELPERKPKT 135
QY 122 LOELRAHENEITKVRKVTENGLOMIVIELGTNPLKSSGIENGAFQGMKKLSYIRADTN 181
DB 136 LOELRAHENEITKVRKVTENGLOMIVIELGTNPLKSSGIENGAFQGMKKLSYIRADTN 195
QY 182 ITSIPQGLPSSLTELHLDGKISRVDASLKGANNLAKGLSPNSISAVDNGSLANTPHL 241
DB 196 ITSIPQGLPSSLTELHLDGKISRVDASLKGANNLAKGLSPNSISAVDNGSLANTPHL 255
QY 242 RELHLDNNKLTTRVPGGLAEHKYIQVYVTLHNNNISVVGSSDFCPGHNTKKAASYGVLSFS 301
DB 256 RELHLDNNKLTTRVPGGLAEHKYIQVYVTLHNNNISVVGSSDFCPGHNTKKAASYGVLSFS 315
QY 302 NPVOYWEIOPSTFRVCYVRSALQLGNY 328
DB 316 NPVOYWEIOPSTFRVCYVRSALQLGNY 342

RESULT 7
5340934-4
Patent No. 5340934
APPLICANT: TERMINE, JOHN D., YOUNG, MARIAN F., FISHER, LARRY W.,
ROBEY, PAMELA G.
TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
NUMBER OF SEQUENCES: 13
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/432,044
FILING DATE: 03-NOV-1989
SEQ ID NO: 4
LENGTH: 353
5340934-4

Query Match 96.5%; Score 1653; DB 6; Length 353;
Best Local Similarity 97.3%; Pred. No. 1.4e-152;
Matches 319; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDDDFEPSLGPVCPFCQCHLRVQCSDDLGLDKVPKOLPDDTLLDLONN 61
DB 26 EASGIGPEVDDDDFEPSLGPVCPFCQCHLRVQCSDDLGLDKVPKOLPDDTLLDLONN 85
QY 62 KITEIKDGDPRKLNKNHALILVNNKISKVSPGAFPLVKLERLYLSKNQKELPERKPKT 121
DB 86 KITEIKDGDPRKLNKNHALILVNNKISKVSPGAFPLVKLERLYLSKNQKELPERKPKT 145
QY 122 LOELRAHENEITKVRKVTENGLOMIVIELGTNPLKSSGIENGAFQGMKKLSYIRADTN 181
DB 146 LOELRAHENEITKVRKVTENGLOMIVIELGTNPLKSSGIENGAFQGMKKLSYIRADTN 205
QY 182 ITSIPQGLPSSLTELHLDGKISRVDASLKGANNLAKGLSPNSISAVDNGSLANTPHL 241
DB 206 ITSIPQGLPSSLTELHLDGKISRVDASLKGANNLAKGLSPNSISAVDNGSLANTPHL 265
QY 242 RELHLDNNKLTTRVPGGLAEHKYIQVYVTLHNNNISVVGSSDFCPGHNTKKAASYGVLSFS 301
DB 266 RELHLDNNKLTTRVPGGLAEHKYIQVYVTLHNNNISVVGSSDFCPGHNTKKAASYGVLSFS 325

QY 302 NPVOYMEIOPSTFRCVYVSATQGNK 329
DB 326 NPVOYMEIOPSTFRCVYVSATQGNK 353

RESULT 8

US-08-442-063A-48
Sequence 48, Application US/08442063A
Patent No. 5705609
GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: PIERSCHBACHER, MICHAEL D.
APPLICANT: CARDENAS, JOSE
APPLICANT: CRAIG, WILLIAM
APPLICANT: MULLEN, DANIEL G.
TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF
TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,063A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,652
FILING DATE: 03-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1454
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-442-063A-48

Query Match 91.5%; Score 1567; DB 1; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.7e-144; Indels 0; Gaps 0;
Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 BASGIGPEVDDRDPEPSIGPVCPFRCCOCHLRVVOCSDLGLDKVPKDLPPDTLLDLQNN 61
DB 4 BASGIGPEVDDRDPEPSIGPVCPFRCCOCHLRVVOCSDLGLDKVPKDLPPDTLLDLQNN 63
QY 62 KITTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLELYLSKNQKELPEKMPKT 121
DB 64 KITTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLELYLSKNQKELPEKMPKT 123
QY 122 LOELRAHENEITVRKVTFNGLNQMTVIELGTNPLKSSGIEGNGAFQGMKKLSYIRIADTN 181
DB 124 LOELRAHENEITVRKVTFNGLNQMTVIELGTNPLKSSGIEGNGAFQGMKKLSYIRIADTN 183
QY 182 ITSIPQGLPSPSLTELHLDGNKISRVDASLKGILNNLAKLGLSFNSISAVDNGSLANTPHL 241
DB 184 ITSIPQGLPSPSLTELHLDGNKISRVDASLKGILNNLAKLGLSFNSISAVDNGSLANTPHL 243

QY 242 RELHLDNNKLTFRVPGGLAEHKYIQVYLLHNNNISVWSSDPCPPGHNTKASYSVGSLSFS 301
DB 244 RELHLDNNKLTFRVPGGLAEHKYIQVYLLHNNNISVWSSDPCPPGHNTKASYSVGSLSFS 303
QY 302 NP 303
DB 304 NP 305

RESULT 9

US-08-442-063A-45
Sequence 45, Application US/08442063A
Patent No. 5705609
GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: PIERSCHBACHER, MICHAEL D.
APPLICANT: CARDENAS, JOSE
APPLICANT: CRAIG, WILLIAM
APPLICANT: MULLEN, DANIEL G.
TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF
TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,063A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,652
FILING DATE: 03-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1454
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-442-063A-45

Query Match 83.7%; Score 1433; DB 1; Length 282;
Best Local Similarity 100.0%; Pred. No. 2.6e-131; Indels 0; Gaps 0;
Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 BASGIGPEVDDRDPEPSIGPVCPFRCCOCHLRVVOCSDLGLDKVPKDLPPDTLLDLQNN 61
DB 4 BASGIGPEVDDRDPEPSIGPVCPFRCCOCHLRVVOCSDLGLDKVPKDLPPDTLLDLQNN 63
QY 62 KITTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLELYLSKNQKELPEKMPKT 121
DB 64 KITTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLELYLSKNQKELPEKMPKT 123
QY 122 LOELRAHENEITVRKVTFNGLNQMTVIELGTNPLKSSGIEGNGAFQGMKKLSYIRIADTN 181
DB 124 LOELRAHENEITVRKVTFNGLNQMTVIELGTNPLKSSGIEGNGAFQGMKKLSYIRIADTN 183
QY 182 ITSIPQGLPSPSLTELHLDGNKISRVDASLKGILNNLAKLGLSFNSISAVDNGSLANTPHL 241

Db 184 ITSLPQGLPESLTLEHLDGKISRVDASLKGNNLAKLGSFNSISAVDNGSLANTPHL 243
QY 242 RELHLDNNKLTFRVPGSLAEHKYIOVYVLHNNISVGS 279
Db 244 RELHLDNNKLTFRVPGSLAEHKYIOVYVLHNNISVGS 281

RESULT 10
US-08-442-063A-42
Sequence 42, Application US/08442063A
Patent No. 5705609
GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: PIERSCHACHER, MICHAEL D.
APPLICANT: CARDENAS, JOSE
APPLICANT: CRAIG, WILLIAM
APPLICANT: MULLEN, DANIEL G.
TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF
TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,063A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,652
FILING DATE: 03-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATRYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1454
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-442-063A-42

Query Match 69.2%; Score 1186; DB 1; Length 236;
Best Local Similarity 100.0%; Pred. No. 2, 1e-107; Indels 0; Gaps 0;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EASGIGREVDDBDFEBSLGPVCPFRQCHLRVVOCSDLGLDKYKQDLPPTTLDDLQNN 61
Db 4 EASGIGREVDDBDFEBSLGPVCPFRQCHLRVVOCSDLGLDKYKQDLPPTTLDDLQNN 63
QY 62 KITREIDGDFKNTKNTLHLLVNNKISKVSFGAFTPLVKLERLYLSNQKELPERKPKT 121
Db 64 KITREIDGDFKNTKNTLHLLVNNKISKVSFGAFTPLVKLERLYLSNQKELPERKPKT 123
QY 122 LOELRAHENEITVYKATYFNGLNQMTVIELGTNPLKSSGIEGNGAFQGMKLSYIRIADTN 181
Db 124 LOELRAHENEITVYKATYFNGLNQMTVIELGTNPLKSSGIEGNGAFQGMKLSYIRIADTN 183
QY 182 ITSLPQGLPESLTLEHLDGKISRVDASLKGNNLAKLGSFNSISAVDN 232

Db 184 ITSLPQGLPESLTLEHLDGKISRVDASLKGNNLAKLGSFNSISAVDN 234

RESULT 11
US-08-303-238-3
Sequence 3, Application US/08303238
Patent No. 5654270
GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: LONGAKER, MICHAEL T.
APPLICANT: WHITBY, DAVID J.
APPLICANT: HARPER, JOHN R.
APPLICANT: PIERSCHACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,238
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: P-LA 9453
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-303-238-3

Query Match 56.4%; Score 966; DB 1; Length 368;
Best Local Similarity 56.5%; Pred. No. 1e-85; Indels 2; Gaps 2;
Matches 186; Conservative 51; Mismatches 90; Indels 2; Gaps 2;
QY 2 EASGIGRE-VPDRDFEBSLGPVCPFRQCHLRVVOCSDLGLDKYKQDLPPTTLDDLQNN 60
Db 40 EASGADTSGVLDPDSVTPTYSAMCPGCHCHLRVVOCSDLGLKSVKEISPTTLDDLQNN 99
QY 61 NITTELRKDDFENKNTKNTLHLLVNNKISKVSFGAFTPLVKLERLYLSNQKELPERKPKT 120
Db 100 NITTELRKDDFENKNTKNTLHLLVNNKISKVSFGAFTPLVKLERLYLSNQKELPERKPKT 159
QY 121 LOELRAHENEITVYKATYFNGLNQMTVIELGTNPLKSSGIEGNGAFQGMKLSYIRIADTN 180
Db 160 SLVEARLHNNRIRKYPNGVFGSLRMNCCLEMGNPLNNGFPGAFDGL-KANTYLRISIA 218
QY 181 NITSLPQGLPESLTLEHLDGKISRVDASLKGNNLAKLGSFNSISAVDNGSLANTPH 240
Db 219 KITGIPKQDLPPTTLLEHLDGKISRVDASLKGNNLAKLGSFNSISAVDNGSLANTPH 278
QY 241 ITSLPQGLPESLTLEHLDGKISRVDASLKGNNLAKLGSFNSISAVDN 232

Db 279 LRELHLDNNKLAARVPSGLPDLKLLQVYVYLSNNITKVGVDPCPMGFVGRAYNGISLFP 338
Qy 301 SNPOVYWEIOPSTFRCCVYRSALQLGNYK 329
Db 339 NNPPYWEVOPATFRCTVDRALAIQFGNYK 367

RESULT 12
US-08-834-3
Sequence 3, Application US/08458834
Patent No. 6277812
GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: LONGAKER, MICHAEL T.
APPLICANT: WHITBY, DAVID J.
APPLICANT: HARPER, JOHN R.
APPLICANT: PIRSCHBACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,834
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: P-LA 9453
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-834-3

Query Match 56.4%; Score 966; DB 3; Length 368;
Best Local Similarity 56.5%; Pred. No. 1e-85;
Matches 186; Conservative 51; Mismatches 90; Indels 2; Gaps 2;

Db 2 EASGIGPE-VPDRDPEPSLGPVCFRCOCHLRVQCSLDGLDKVPKDLPPDTLLDLOV 60
Db 40 EASGADTSGVLDDPSVPTYSAMCPFGCHLRVQCSLDGLKSVPEISPTDILLDLOV 99
Qy 61 NKTTEIKDGPFKNLKHALILVNNKISKVSPGAFPTVLERLYSKNQKELPERMPK 120
Db 100 NDISERKDDPKGLQHLVYALVLYNNKISKIHEKAFSLRVQKLYISKHNLVEIPPLPS 159
Qy 121 TLQELAHENEITKRVKVTENGNGMNVILGTPNPKSSGIGENARQGMKGLSYIRIADT 180
Db 160 SLVELRKHDRIRKRVNGVSGLRNNKCIEMGGPLENSGEPGAFGL-KLNYLRISEA 218
Qy 181 NITSIPQGLPPSTLTELHLDGKISRVDASILKGLNNLAKGLSFNSISAVDNGSLANTPH 240

Db 219 KLTIKPKDLPTLNLHLDHNNKIQAILEDLRLYSKLYRLGLGHQNIIRMENGLSFLPT 278
Qy 241 LRELHLDNNKLTFRVPGGLAEHKYIQVYVYLNHNNISVVGSSDPEPPGHNTKKSYSGVSLF 300
Db 279 LRELHLDNNKLAARVPSGLPDLKLLQVYVYLSNNITKVGVDPCPMGFVGRAYNGISLFP 338
Qy 301 SNPOVYWEIOPSTFRCCVYRSALQLGNYK 329
Db 339 NNPPYWEVOPATFRCTVDRALAIQFGNYK 367

RESULT 13
5340934-2
Patent No. 5340934
APPLICANT: TERKINE, JOHN D.; YOUNG, MARIAN F.; FISHER, LARRY W.
APPLICANT: ROBERT, PAMELA G.
TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
NUMBER OF SEQUENCES: 13
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/432,044
FILING DATE: 03-NOV-1989
SEQ ID NO: 2
LENGTH: 368
5340934-2

Query Match 56.3%; Score 965; DB 6; Length 368;
Best Local Similarity 56.2%; Pred. No. 1.3e-85;
Matches 185; Conservative 53; Mismatches 89; Indels 2; Gaps 2;

Qy 2 EASGIGPE-VPDRDPEPSLGPVCFRCOCHLRVQCSLDGLDKVPKDLPPDTLLDLOV 60
Db 40 EASGADTSGVLDDPSVPTYSAMCPFGCHLRVQCSLDGLKSVPEISPTDILLDLOV 99
Qy 61 NKTTEIKDGPFKNLKHALILVNNKISKVSPGAFPTVLERLYSKNQKELPERMPK 120
Db 100 NDISERKDDPKGLQHLVYALVLYNNKISKIHEKAFSLRVQKLYISKHNLVEIPPLPS 159
Qy 121 TLQELAHENEITKRVKVTENGNGMNVILGTPNPKSSGIGENARQGMKGLSYIRIADT 180
Db 160 SLVDVRIHNNIRKRVKGVSGLRNNKCIEMGGPLENSGEPGAFGL-KLNYLRISEA 218
Qy 181 NITSIPQGLPPSTLTELHLDGKISRVDASILKGLNNLAKGLSFNSISAVDNGSLANTPH 240
Db 219 KLTIKPKDLPTLNLHLDHNNKIQAILEDLRLYSKLYRLGLGHQNIIRMENGLSFLPT 278
Qy 241 LRELHLDNNKLTFRVPGGLAEHKYIQVYVYLNHNNISVVGSSDPEPPGHNTKKSYSGVSLF 300
Db 279 LRELHLDNNKLAARVPSGLPDLKLLQVYVYLSNNITKVGVDPCPMGFVGRAYNGISLFP 338
Qy 301 SNPOVYWEIOPSTFRCCVYRSALQLGNYK 329
Db 339 NNPPYWEVOPATFRCTVDRALAIQFGNYK 367

RESULT 14
US-08-442-063A-39
Sequence 39, Application US/08442063A
Patent No. 5705609
GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: PIRSCHBACHER, MICHAEL D.
APPLICANT: CARDENAS, JOSE
APPLICANT: CRAIG, WILLIAM
APPLICANT: MULLEN, DANIEL G.
TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF
TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES

ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,063A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/865,652
FILING DATE: 03-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHERYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1454
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-442-063A-39

Query Match 55.3%; Score 948; DB 1; Length 188;
Best Local Similarity 100.0%; Pred. No. 2.1e-84;
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGEVDDDDFEPSLGVPCEFRQCHLRVQCSDLGLDKVPKDLPPDTLLDQNN 61
DB 4 EASGIGEVDDDDFEPSLGVPCEFRQCHLRVQCSDLGLDKVPKDLPPDTLLDQNN 63
QY 62 KITETKGDGFKNLKNTLHLLVNNKISKVSPGAFPLVLERLYLSNQKELPEKMPKT 121
DB 64 KITETKGDGFKNLKNTLHLLVNNKISKVSPGAFPLVLERLYLSNQKELPEKMPKT 123
QY 122 LOELRAHENITKVRKTPFNGLNOMITELGTPNPKSSGIENGAFOGKQLSYIRLDTN 181
DB 124 LOELRAHENITKVRKTPFNGLNOMITELGTPNPKSSGIENGAFOGKQLSYIRLDTN 183
QY 182 ITS 184
DB 184 ITS 186

RESULT 15
US-09-724-864-43
Sequence 43, Application US/09724864
Patent No. 6380362
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Watson, James G.
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
TITLE OF INVENTION: by the polynucleotides and methods for their use.
FILE REFERENCE: 11000.1050U1
CURRENT APPLICATION NUMBER: US/09/724,864
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 43
LENGTH: 373
TYPE: PRT
ORGANISM: Mouse
US-09-724-864-43

Query Match 54.0%; Score 925.5; DB 4; Length 373;
Best Local Similarity 53.7%; Pred. No. 9.3e-82;

Matches 173; Conservative 62; Mismatches 80; Indels 7; Gaps 2;
QY 6 IGPEVDDDDFEPSLGVPCEFRQCHLRVQCSDLGLDKVPKDLPPDTLLDQNNKITE 65
DB 56 VDNFFPPD-----LPPCPFGQCYSRVVHCSDDLTSVNNIPDTRVVDLQNNKITE 109
QY 66 IKDDGPKNLKNTLHLLVNNKISKVSPGAFPLVLERLYLSNQKELPEKMPKTLOEL 125
DB 110 IKENDFGKLSLALILNNKTLKIHKPTFLTKDLRLYLSNQKELPEKMPKTLOEL 169
QY 126 RAHEKITVRKTPFNGLNOMITELGTPNPKSSGIENGAFOGKQLSYIRLDTNITS1 185
DB 170 RHDKNKVKKIQTPTFGNNAHLVLEMSANPLENNGIEPGAFCGV-TVFHIRIAAKLTST1 228
QY 186 PGLPPLSLTEIHDGKISRVAASLKGUNLAKGLSPNSISAVNGSIANTPHLEH 245
DB 229 PKGLPPTLLEHLDKFKISTVELEDKRYRELQRLDGNRRITDINGFANPRVREIH 288
QY 246 LDNNKLRVPGGLAEKVIQVYLIHNNNISVVGSSDFCEPGHNTKASYSGLFSPNPVQ 305
DB 289 LEHNKTKKIPSGIQLKTYIIFLHYNSTAKGVNDFCPTVPKMKSLYSALSPNNPK 348
QY 306 YWEIQSTRCYVVRSAIQDGN 327
DB 349 YWEIQPATFRCVLGRMSVQDGN 370

RESULT 16
US-08-442-063A-36
Sequence 36, Application US/08442063A
Patent No. 5705609
GENERAL INFORMATION:
APPLICANT: RIOSLAHTI, ERKKI I.
APPLICANT: PIRSCHBACHER, MICHAEL D.
APPLICANT: CARDENAS, JOSE
APPLICANT: CRAIG, WILLIAM
APPLICANT: MULLEN, DANIEL G.
TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF
TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,063A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/865,652
FILING DATE: 03-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHERYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1454
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-442-063A-36

Query Match 41.7%; Score 714; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 86-62;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDRDPEFSLGVPVCFRCQCHLRVQCSDLGLDKVPKDLPPDTLLDLQNN 61
DB 4 EASGIGPEVDDRDPEFSLGVPVCFRCQCHLRVQCSDLGLDKVPKDLPPDTLLDLQNN 63
QY 62 KITETKDGDFKKNLKNHALILVNNKISKVSPGAFPLVLERLYLSNQKKEIPKPKPT 121
DB 64 KITETKDGDFKKNLKNHALILVNNKISKVSPGAFPLVLERLYLSNQKKEIPKPKPT 123
QY 122 LOELRAHENEITKVRK 137
DB 124 LOELRAHENEITKVRK 139

RESULT 17

US-08-442-063A-33
; Sequence 33; Application US/08442063A
; Patent No. 5705609
; GENERAL INFORMATION:
; APPLICANT: RIOSLAHTI, ERKKI I.
; APPLICANT: PIERSCHACHER, MICHAEL D.
; APPLICANT: CARDENAS, JOSE
; APPLICANT: CRAIG, WILLIAM
; APPLICANT: MULLER, DANIEL G.
; TITLE OF INVENTION: DECORIN FRAGMENTS AND METHODS OF
; TITLE OF INVENTION: INHIBITING CELL REGULATORY FACTORS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,063A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865,652
; FILING DATE: 03-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHERYN A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-1A 1454
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-442-063A-33

QY 28.5%; Score 488; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 4,3e-40;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 4 EASGIGPEVDDRDPEFSLGVPVCFRCQCHLRVQCSDLGLDKVPKDLPPDTLLDLQNN 63

QY 62 KITETKDGDFKKNLKNHALILVNNKISKVSP 92
DB 64 KITETKDGDFKKNLKNHALILVNNKISKVSP 94

RESULT 18

US-09-188-930-305
; Sequence 305; Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Ornust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000,1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 305.
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Mouse
US-09-188-930-305

Query Match 19.9%; Score 341; DB 3; Length 649;
Best Local Similarity 31.6%; Pred. No. 1,6e-24;
Matches 89; Conservative 49; Mismatches 86; Indels 58; Gaps 9;

QY 24 CPERCQCHLRVQCSDLGLDKVPKDLPPDTLLDLQNNKITETKDGDFKKNLKNHALILV 83
DB 31 CPERCQCHLRVQCSDLGLDKVPKDLPPDTLLDLQNNKITETKDGDFKKNLKNHALILV 81
QY 84 NNTKISKVSPGAFPLVLERLYLSNQKKEIPKPKPTLOELRAHENEITKVRKVTENG 143
DB 82 -----LKVQRIYIYHNSLDEFPNLRKYVELHLOENNT---RTITVDSL 124
QY 144 NQNVIV---LGTNPILKSGIENGAFQGMKQSYIRIADNTITSIPQSLTEHLDG 200
DB 125 SKIPYELHLDNDSVSAVSEIIEGAFRDSVYLLFLSRHLSITPGLPRTIEELRLD 184
QY 201 NTKSRDASLKLGLNLAIGLSFN-----SISAVNGSLA---NT 238
DB 185 NRTISSPSLHGLTSLKRLVLDGNLNNHGLDKVPFNLVNLTELSLVNNSLTAAPVNL 244
QY 239 P-HLEHLDNKNKLTVPVGLAEHKYIOVY---LHNNNIS 275
DB 245 PGTSLKRLVLDNHNIRVPPN--AFSYLRQLYRLDMSNNNIS 284

RESULT 19

US-09-312-283C-305
; Sequence 305; Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Ornust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000,1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 305
; LENGTH: 649

TYPE: PRT
ORGANISM: Mouse
US-09-312-283C-305

Query Match 19.9%; Score 341; DB 4; Length 649;
Best Local Similarity 31.6%; Pred. No. 1.6e-24;
Matches 89; Conservative 49; Mismatches 86; Indels 58; Gaps 9;

QY 24 CPEFCQCHLRVQCSDLGDKVPKDLPPDTLLDQNNKTEIKDGRKLNKLNHALIV 83
DB 31 CPVCRCDAGFYICNDRLSTSI PVGIPEDATTLYLQNNQINN--GISPDGKN----- 81
QY 84 NNNKSVSPGAFPLVKKLELYLSKNQKELPEKPKTLOEBAHEHETIVRKTEGTL 143
DB 82 -----LKKQRIYLYNLSDEEPTNLPKVKSHLQENNI---RTITDGL 124
QY 144 NQMTIV--LGTNPLKSSGIENGAFQGMKLSYIRIADTITSIPQGLPSLTLEHLDG 200
DB 125 SKIPLLEHLDNDSVSAVSIIEGAFRDSNTLRLLFLSRNHLSTIPGLPRTIELRLDD 184
QY 201 NKISRVDAASLKGNNLAKLGLSPY-----SISAVDNGSLA---NT 238
DB 185 NRIITSSPSLHGLTSLKRLVLDGTLNNGHGDGVFNVLVLTSLVRSNLTAPVNL 244
QY 239 P--HLEHLDNNKLTFRVPGGLAEHKYIQVY---LHNNNIS 275
DB 245 PGTSLRKLYLDQNNHINRVPPN--AFSYLKQILRDMNNNIS 284

RESULT 20

US-08-303-238-1
Sequence 1, Application US/08303238
Patent No. 5654270

GENERAL INFORMATION:

APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: LONGAKER, MICHAEL T.
APPLICANT: WHITBY, DAVID J.
APPLICANT: HARPER, JOHN R.
APPLICANT: PIERSEBACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,238
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: P-LA 9453
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-8949
TELEFAX: 619-535-9001
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-303-238-1

Query Match 19.1%; Score 326.5; DB 1; Length 376;
Best Local Similarity 27.9%; Pred. No. 1.8e-23;
Matches 91; Conservative 64; Mismatches 146; Indels 25; Gaps 8;

QY 8 PEVDDRDPEFSPSLAPVCPFRQC--HRRVQCSDLGDKVPKDLPPDTLLDQNNKIT 64
DB 68 PSPDPDPD-----CPQECDCPPNFLTAMYCDNRMLKYLFP--FVPSMRKVVYFQNNQIT 118
QY 65 EIKQDGRKLNKLNHALIVNNKIS--KVSPPAFPLVKKLELYLSKNQKELPEKPKETL 122
DB 119 SIQGVFDNATGTLIMLHNGQITSDYGRKVFSLHLELYLDHNNLTETMPGPLPSL 178
QY 123 QELFAHNEITKVKAFVFNGLNQMIVIELGTNPKSSGIENGAFQGMKLSYIRIADTNI 182
DB 179 RELHLDNQISRVNNMLEGENTLALYLQHDEIQEVG---SSMRGLSLILDLSTNHL 235
QY 183 TSIPQGLPSLTLEHLDGKNTSRVDAASLKGNNLAKLGLSPNSISAVDNGSLANT--P 239
DB 236 RKVPDGLPSALBQLYMEHNNVYTPDSYFRGAPKLLYVRLSHNSLT--NNGLASNTENS 293
QY 240 HLEHLDNNKLTFRVPGGLAEHKYIQVYLLHNNISVVGSSDFCPGHNTKKASVGSYL 299
DB 294 SLLELDLSYNQLOKIP--PVNTMLENLYLQGNINBFSISSFCTVVDVYVNSKIQVRL 350
QY 300 FSNPQYWEIOPSTFRGVVRSATQL 325
DB 351 DGNKIKSAMPADAPLCRLASLIEI 376

RESULT 21

US-08-458-834-1
Sequence 1, Application US/08458834
Patent No. 6277812

GENERAL INFORMATION:

APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: LONGAKER, MICHAEL T.
APPLICANT: WHITBY, DAVID J.
APPLICANT: HARPER, JOHN R.
APPLICANT: PIERSEBACHER, MICHAEL D.
APPLICANT: BORDER, WAYNE A.
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY FACTORS
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR REDUCING SCARRING
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,834
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: P-LA 9453
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 376 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-834-1

Query Match 19.1%; Score 326.5; DB 3; Length 376;
Best Local Similarity 27.9%; Pred. No. 1.8e-23;
Matches 91; Conservative 64; Mismatches 146; Indels 25; Gaps 8;

QY 8 PEVDDRDPEPSLGPVCPFCQC--HLRVQCSDLGLDKVPKDLPPDTLLDQNNKIT 64
DB 68 PEPDPFRD-----CPQECDEPPIFLTAMVCDNNRLKLP-FVPSRMKMYVVFQNNQIT 118
QY 65 EIKDGFRLKULHALLIVNNKIS--KVPGATPLVLEKRLYLSKNQKELPEKMPKT 122
DB 119 SIQGVFNATGTLMTALHGNQITSDKVGKVFYSKLRHLRLYLDHNNITRMGPLPRSL 178
QY 123 QELAHENITKRVKTYFNGLNQMIIVIELGTNPDKSGGIENGAFQGMKLSYRIADTN 182
DB 179 RELHLDHNOISRPNNALEGLNTALYLQHDIEQVG--SSMRGLRSLILDLISYNH 235
QY 183 TSIPQGLPSSLTEHLHDGNKISRVDASLKLNNLAKLGLSFNSISAVDNGSLANT---P 239
DB 236 RKVPDGLPSALEGLVMEHNVTVPDPSYFRGAKPLLYVRSNLSLT--NNGLASNTPFNS 293
QY 240 HRELHLDNNKLTFRVGGLAHEKTYIQVYILANNISVVGSSDCPPGHNTKASISGVSL 299
DB 294 SLELDLSYNOLOKIP---PVNTNLENLYLQGNRINEFSSISPTVVDVVFSLQVYRL 350
QY 300 FSNPVQYMEIQPSTFRGVVRSALOL 325
DB 351 DGNETKRSAMPADAPLCRLASLIEI 376

RESULT 22

US-09-191-647-7
; Sequence 7, Application US/09191647
; Patent No. 6046015
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kild, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/191,647
; EARLIER FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: 60/065,544
; EARLIER FILING DATE: 1997-11-14
; EARLIER APPLICATION NUMBER: 60/081,057
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1480
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-191-647-7

Query Match 18.9%; Score 323; DB 3; Length 1480;

Best Local Similarity 25.3%; Pred. No. 3.2e-22;
Matches 99; Conservative 61; Mismatches 129; Indels 102; Gaps 9;

QY 2 EASGIEPEVDDRDPEPSLGPVCPFCQCCHLRVQCSDLGLDKVPKDLPPDTLLDQNN 61
DB 277 KCSGLTEHAPMEGAGENS-----CPHRCRCDGIVDCREKSLTSVPYTLPPDITDVALQON 332
QY KITEIKDGFRLKULHALLIVNNKISKVSPGAFPLVLEKRLYLSKNQKELPEKMPKT 121
DB 62 KITEIKDGFRLKULHALLIVNNKISKVSPGAFPLVLEKRLYLSKNQKELPEKMPKT 121
DB 333 FITELPPKSFSSFRRLRIDLSNNNISRIAHDLASGLKQLTTLVLYGNKIKDLPQGVFKG 392

QY 122 LOELR---AHENETKRVKTYFNGLNQMIIVIELGTNPDKSGGIENGAFQGMKLSYRI 178
DB 393 LGSIRLLNANNEISICIRDAFRDLSLSLYDNNIOS--LANGTFAMKSMKTVHLA 450
QY 179 -----DTN----- 181
DB 451 KNPFICDNLRLADYLAHNPRIETSGARCESPRMRRRIEISIREKFKCSWGLRMKLS 510
QY 182 -----ITSIPQGLPSSLTEHLHDGNKISRVDASLKG-L 214
DB 511 GECRMDSDCPAMCHCEGTTVDCTGRRRLKEIPDIPATTELLINDNEIGRISDGLPRL 570
QY 215 NNILAKLGSFNSISAVDNGSLANTPHLREHLHDNNKLTFRVPG--LAHEKTYIQVYILANN 272
DB 571 PHVYLELRKNQLTGIEHPAFEGASHIQELQGENKIKISNMFLGLHQ-LKTLNLYDN 629
QY 273 NISVVGSSDPCPPGHNTKASISGVSLFSPN 303
DB 630 QISCV-----MGSFEHLNLSLTSLNASNP 654

RESULT 23

US-09-540-245A-7
; Sequence 7, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kild, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; EARLIER FILING DATE: 2000-03-31
; EARLIER APPLICATION NUMBER: 60/065,544
; EARLIER FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1480
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-540-245A-7

Query Match 18.9%; Score 323; DB 3; Length 1480;
Best Local Similarity 25.3%; Pred. No. 3.2e-22;
Matches 99; Conservative 61; Mismatches 129; Indels 102; Gaps 9;

QY 2 EASGIEPEVDDRDPEPSLGPVCPFCQCCHLRVQCSDLGLDKVPKDLPPDTLLDQNN 61
DB 277 KCSGLTEHAPMEGAGENS-----CPHRCRCDGIVDCREKSLTSVPYTLPPDITDVALQON 332
QY 62 KITEIKDGFRLKULHALLIVNNKISKVSPGAFPLVLEKRLYLSKNQKELPEKMPKT 121
DB 333 FITELPPKSFSSFRRLRIDLSNNNISRIAHDLASGLKQLTTLVLYGNKIKDLPQGVFKG 392
QY 122 LOELR---AHENETKRVKTYFNGLNQMIIVIELGTNPDKSGGIENGAFQGMKLSYRI 178
DB 393 LGSIRLLNANNEISICIRDAFRDLSLSLYDNNIOS--LANGTFAMKSMKTVHLA 450
QY 179 -----DTN----- 181
DB 451 KNPFICDNLRLADYLAHNPRIETSGARCESPRMRRRIEISIREKFKCSWGLRMKLS 510
QY 182 -----ITSIPQGLPSSLTEHLHDGNKISRVDASLKG-L 214
DB 511 GECRMDSDCPAMCHCEGTTVDCTGRRRLKEIPDIPATTELLINDNEIGRISDGLPRL 570
QY 215 NNILAKLGSFNSISAVDNGSLANTPHLREHLHDNNKLTFRVPG--LAHEKTYIQVYILANN 272

Db 571 PHVLKELKKNQLTGIEPNNAFEGASHIQEOLGKNTKEISNKNMGLHQ-LKTLNLYDN 629
Qy 273 NISVGSDDPCPGHNTKASYSVSLFSPN 303
Db 630 QISCV-----MPGSFEHLNLSLTSLNLSNP 654

RESULT 24
US-09-540-153-7
Sequence 7, Application US/09540153
Patent No. 6270995
GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Kid, Thomas
APPLICANT: Brose, Katja
APPLICANT: Teessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,153
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/191,647
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/081,057
PRIOR FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 1480
TYPE: PRP
ORGANISM: Drosophila melanogaster
US-09-540-153-7

Query Match 18.9%; Score 323; DB 3; Length 1480;
Best Local Similarity 25.3%; Pred. No. 3.2e-22;
Matches 99; Conservative 61; Mismatches 129; Indels 102; Gaps 9;
Qy 2 EASGIGPEVDDRDPEPSLGPVCFRCQCHLRVQCSDLGLDKVPKDLPPDTLLDLONN 61
Db 277 KCSGLTEHAPMEGCAENS-----CPHPCRCADGIVDCREKSLTSVPVTLPPDTTIDVRLQON 332
Qy 62 KITEIKDGFKNLKNLHALLVNNKISKVSPGAFPLVLERLYLSKNQKLELPERKPKT 121
Db 333 FTTELPPKSFSSFRRLRRIDLSNNNISRIAHALSGKQKTLTVLVGNKIKDLPSSGVFKG 392
Qy 122 LOELR---AHENETTKRVKVTNGLNQMIIVIELGTNPLKSSGIEGNAFGMKKLSYIRIA 178
Db 393 LGSIRLLILNANEISCIKDAFRDLHSLSLSTLYDNNIQS--LANTGTFAMKSKTVHLA 450
Qy 179 -----DTN----- 181
Db 451 KNPFICDCLRWLADVLHKNPITSGARCSPKMRHRRILESLEKFKCSGELRMKLS 510
Qy 182 -----ITSIPQGLPSELTEHLHDGKNTKISVDAASLKG-L 214
Db 511 GECRMDSDCPAMCHCEGTVDCTGRRLEKEIPRDIPLHTTELLNDNEIGRISISDGLFGR 570
Qy 215 NNLAKLGLSPNSISAVDNGSLANTPHLREHLNNDKLTTRVPGG--LAENKCYQVNYLANN 272
Db 571 PHVLKELKKNQLTGIEPNNAFEGASHIQEOLGKNTKEISNKNMGLHQ-LKTLNLYDN 629
Qy 273 NISVGSDDPCPGHNTKASYSVSLFSPN 303
Db 630 QISCV-----MPGSFEHLNLSLTSLNLSNP 654

RESULT 25
PCT-US91-09055-2
Sequence 2, Application PC/TUS9109055
GENERAL INFORMATION:
APPLICANT: Rohberg, Jonathan Marc and Artavanis-Tsakonas, Spyridon
TITLE OF INVENTION: Purified slit protein and Sequence Elements Thereof
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:

ADDRESSEE: Yale University
ADDRESSEE: Office of Cooperative Research
STREET: 246 Church Street
STREET: Suite 401
CITY: New Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06510
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/09055
FILING DATE: 19911127
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/624,135
FILING DATE: 7-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barth, Richard J.
REGISTRATION NUMBER: 28,180
REFERENCE/DOCKET NUMBER: 900964/RSB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 972-1400
TELEFAX: (212) 370-1622
TELEX: 236268
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1480 amino acids
TYPE: AMINO ACIDS
TOPOLOGY: Linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: 1 to 36
IDENTIFICATION METHOD: similarity to other signal
OTHER INFORMATION: Directs Export
NAME/KEY: Four Plank-LRR-Plank domains
LOCATION: 37 to 910
IDENTIFICATION METHOD: Array of Plank-LRR-Plank
OTHER INFORMATION: mediates adhesive events
NAME/KEY: Tandem EGF-like repeats
LOCATION: 911 to 1150
IDENTIFICATION METHOD: similarity to tandem EGF-like
OTHER INFORMATION: protein-protein interactions
NAME/KEY: 7th EGF-like repeat
LOCATION: 1353 to 1393
IDENTIFICATION METHOD: similarity to epidermal growth
OTHER INFORMATION: Involvement in receptor-ligand
NAME/KEY: Alternative splice segment
LOCATION: 1394 to 1404
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: developmentally regulated
NAME/KEY: COOH-terminal region
LOCATION: 1405 to 1480
IDENTIFICATION METHOD: experimental
PCT-US91-09055-2
Query Match 18.9%; Score 323; DB 5; Length 1480;
Best Local Similarity 25.3%; Pred. No. 3.2e-22;
Matches 99; Conservative 61; Mismatches 129; Indels 102; Gaps 9;
Qy 2 EASGIGPEVDDRDPEPSLGPVCFRCQCHLRVQCSDLGLDKVPKDLPPDTLLDLONN 61
Db 277 KCSGLTEHAPMEGCAENS-----CPHPCRCADGIVDCREKSLTSVPVTLPPDTTIDVRLQON 332
Qy 62 KITEIKDGFKNLKNLHALLVNNKISKVSPGAFPLVLERLYLSKNQKLELPERKPKT 121
Db 333 FTTELPPKSFSSFRRLRRIDLSNNNISRIAHALSGKQKTLTVLVGNKIKDLPSSGVFKG 392
Qy 122 LOELR---AHENETTKRVKVTNGLNQMIIVIELGTNPLKSSGIEGNAFGMKKLSYIRIA 178

```

Db      393 LGSRLILNNANNEISCRKQAFRLHSLSLSDNNIQS--LANGTDMANKMKTATLA 450
      179 -----DTN----- 181
Db      451 KNPFLCDNRLWADYLHKNPLETSGARCESPKRMRHRRISLEBEKFKCSWGLRMGLS 510
      182 -----ITSIPQGLPPLSTTEHLHDGKISRVDASLKG-L 214
Db      511 GECRMDSCPPAMCHCEGTTVDCTGRRLKEIPRDIPLHTELLDNLGRISSDGLFGRLL 570
      215 NNLAALGLSFNSISAVDNGSLANTPHRLHLDNNKLTFRVPG--LAEHKTYIOVVYLIANN 272
      571 PHLVLTGLKRNQQLTIEBNAFEGASHIQLGKIKKISNKNFLGLHQ-LKTLNLYDN 629
      273 NISVVGSSDFCPGHNTHKASYSVGLFSNP 303
      630 QISCY-----MPGSFHLNLSLTSLNLSNP 654

RESULT 26
US-09-182-024A-5
; Sequence 5, Application US/09182024A
; Patent No. 6342370
; GENERAL INFORMATION:
; APPLICANT: Connolly, Timothy
; APPLICANT: Rajput, Bhannu
; TITLE OF INVENTION: Human slit Polypeptide and Polynucleotides Encoding
; FILE REFERENCE: 640100-271
; CURRENT APPLICATION NUMBER: US/09/182,024A
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/063,946
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/096,420
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1480
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-182-024A-5

Query Match      18.7%; Score 321; DB 4; Length 1480;
Best Local Similarity 25.3%; Pred. No. 4.9e-22;
Matches 99; Conservative 61; Mismatches 129; Indels 102; Gaps 9;

      2 EASGIGPEVPDRDRPEPLGVCPRCCCHLRVVOCSLGLDKYPKDLPPDTLLDQNN 61
      277 KCSGTEHAPMECGAENS---CPHPCACADGIVDCREKSLTSVAVTLPPDTTLYLLEON 332
      62 KITEIKDGFKNLKNLHLLIVNNKISVSPGAFPLVKLERLYLSKQQLKELPEKMKPT 121
      333 FITEIPPSFSFRLRIRIDISNNNISRIANDASLGLQTLTLYLYGKIKITDPSGVKXG 392
      122 LQELR---AHENETKYRKVTFENGINQMIIVIELGTNPDKSSGIENGAFQGMKKLSYIRIA 178
      393 LGSRLILNNANNEISCRKQAFRLHSLSLSDNNIQS--LANGTDMANKMKTATLA 450
      179 -----DTN----- 181
      451 KNPFLCDNRLWADYLHKNPLETSGARCESPKRMRHRRISLEBEKFKCSWGLRMGLS 510
      182 -----ITSIPQGLPPLSTTEHLHDGKISRVDASLKG-L 214
      511 GECRMDSCPPAMCHCEGTTVDCTGRRLKEIPRDIPLHTELLDNLGRISSDGLFGRLL 570
      215 NNLAALGLSFNSISAVDNGSLANTPHRLHLDNNKLTFRVPG--LAEHKTYIOVVYLIANN 272
      571 PHLVLTGLKRNQQLTIEBNAFEGASHIQLGKIKKISNKNFLGLHQ-LKTLNLYDN 629
      273 NISVVGSSDFCPGHNTHKASYSVGLFSNP 303

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Db      630 QISCY-----MPGSFHLNLSLTSLNLSNP 654

RESULT 27
US-09-312-283C-396
; Sequence 396, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Ormest, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 396
; LENGTH: 1529
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-396

Query Match      18.7%; Score 321; DB 4; Length 1529;
Best Local Similarity 25.4%; Pred. No. 5.2e-22;
Matches 105; Conservative 60; Mismatches 130; Indels 118; Gaps 12;

      10 VPDDRDFEPLGIP-----VCPRCQCHLRVVOCSLGLDKVPKDLPPDTLLDQNNKI 63
      486 IPGTEDYRSKLSGDCFADLACPEKRCCEGTTVDCCSNQKMKIPDHIPQYTAELRINNNEF 545
      64 TEIK-DDEPKNLKNLHLLIVNNKISVSPGATPLVKLERLYLSKQQLKELPEKMKPTL 122
      546 TVLEATGIFPKKLPLQRKINISNNKITDIEGAFEGASGVNEILLTSRLNVOHKMKGL 605
      123 QELRA-----HENETKYRKVTFENGINQMIIVIELGTNP 155
      606 ESKLTMLRNSNRISCVGNDSTGLGVSRLSLSDNNIQTLYAPGAFGLHSLSLNLSNP 665
      156 -----LKSSGIENGAFQ-----GMKKLS 173
      666 FNCHCHLAWIGEMLRRIYTGPNRCQKPYFLAKEIPIDVAILQDFTCDGNDGNSCPLS 725
      174 -----YIRIADTNITSIPQGLPPLSTTEHLHDGKISRVDASLGLNNAALKGL 222
      726 RCPSECTCLDPTVVRCSNKGKLVLPKGIPRDVTLEYLDGNOFTLYV-PRELSNYKHLTLIDL 784
      223 SFNSISAVDNGSLANTPHRLHLDNNKLTFRVPG--GLAEHKTYIOVVYLIANNISVVG 278
      785 SNNISISTLSNQSRSNMTQTLTLLISYRLKICIPRTFDGL---KSLLSLSHGNDISVV- 840
      279 SSDFCPGHNTHKASYSVGLFSNPV-----QYWEIOPSTFRC 316
      841 -----PEGAGDLSALSHLAIAGNPLVCCDGNMGLSDWVYSEYKE--PGIARC 886

RESULT 28
US-09-182-024A-2
; Sequence 2, Application US/09182024A
; Patent No. 6342370
; GENERAL INFORMATION:
; APPLICANT: Connolly, Timothy
; APPLICANT: Rajput, Bhannu
; TITLE OF INVENTION: Human slit Polypeptide and Polynucleotides Encoding
; FILE REFERENCE: 640100-271
; CURRENT APPLICATION NUMBER: US/09/182,024A
; PRIOR FILING DATE: 1998-10-23

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: PRIOR APPLICATION NUMBER: 60/063,946
: PRIOR FILING DATE: 1997-10-31
: PRIOR APPLICATION NUMBER: 60/096,420
: PRIOR FILING DATE: 1998-08-13
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 1523
: TYPE: PRN
: ORGANISM: Homo sapiens
: US-09-182-024A-2

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Query Match	18.7%;	Score 320;	DB 4;	Length 1523;
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OY      23 VCPFFCQCHLRVVOCSDLGKVPKDPDLPDPTLLDLONNKITEIK-DGCFKULKNLHAI 81
Db      504 VCPECKRCGGTTVDOSNQVLRIPEHLPEYVDLRLINDEVSVLERTGIFKFLPNLRKTN 563
OY      82 LVNNKISKVSGAFPTVLKERTLYUSKNQKELPEKMPKTLQELRA---HENEITVRKV 138
Db      564 LSNKKIKKVRBEAFFGAASVOELMTGNQLETVHGRVFGLSGLKTLMLRSLNISCVSND 623
OY      139 TENGINQMIVIELGTN----- 154
Db      624 TPAGLSSVRLSLYDNRIITTPGAFTLLVSPVHHKRPVQPLQLOPLMLGKMLRKRI 663
OY      155 -----PLKSSGIENGAFQGMKLS-----YIRLADTVI 182
Db      664 VSGNRCCKPFELKEIPIODVAIODFTCPGNBESSCOLSPRCPEOCTMEATVRCSENKL 743
OY      183 TSIPOGLPSPSLFELHLDGKISGRVAAASIKGLNNLAKGLSPNSISAVNGSLANPPIHR 242
Db      744 RALPEGMPEVDVETELTEGHNHTAV-PRFESALRHLLTILDSNNISISMLTNYTFSSNHSLS 802
OY      243 ELHLDNNKLTVP-----GGLAEHKYIQVYVLIHNNNISVVGSSDFCPGHNATKKAASYSGVS 298
Db      803 TLILSYNLRRCIPVAHANGL---RSLRLVTLIHGNDISSV-----PEGSFNDLTLSHLA 653
OY      299 LFSNPV 304
Db      854 LGTNPL 859

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RESULT 29
US-09-191-647-2

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: GENERAL INFORMATION:
: APPLICANT: Goodman, Corey
: APPLICANT: Kid, Thomas
: APPLICANT: Brose, Katja
: APPLICANT: Tebster-Layagne, Marc
: TITLE OF INVENTION: Modulating Robo: Ligand Interactions
: FILE REFERENCE: B98-031-3
: CURRENT APPLICATION NUMBER: US/09/191,647
: CURRENT FILING DATE: 1998-11-13
: EARLIER APPLICATION NUMBER: 60/065,544
: EARLIER FILING DATE: 1997-11-14
: EARLIER APPLICATION NUMBER: 60/081,057
: EARLIER FILING DATE: 1998-04-07
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 1525
: TYPE: PRT
: ORGANISM: human
US-09-191-647-2

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Query Match	18.5%;	Score 317;	DB 3;	Length 1525;
Best Local Similarity	25.7%;	Pred. No. 1.3e-21;		
Matches 101; Conservative	60;	Mismatches 120;	Indels 112;	Gaps 11;

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QY      24  CPEFCQGHLYAVGSSDGLADKVPKDLPRDITLLDIQNNKITEIK-DGDEKRIKNIHALLL 82
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QY      83  VNNKISKVSPGAFITVLKLERLYLSKNOLKELPEKMPKTLQELRA----- 127
Db      562  SNNKITDLBEAGFBGASGVNELLTNSNLEENQHHQMPKGBELKTLMLRSNRIITCVGNS 621
QY      128  -----HENETIKVRKVTENGANQMI VIELGTFP----- 155
Db      622  FIGHSSVLLSLYNDQITTTVA BGAEDTILHSITLMIANPENCYLAWIGEWLRKRRTIV 681
QY      156  -----LKSSGIENGAFQ-----GKKKLS-----YIRIADTNI 182
Db      682  TGNPRCQKPYFELKEIPIDVVAI QDFTCDGDGNDNSCSPISRCPTTECTCLADTVVRCNNKGL 741
QY      183  TSIPOGLPEPSLTLELHDGKISRVAASIKGLINNLAKLGLSPNISIAVNGSILANP.PHLR 242
Db      742  KVLPRKGIIRDVTEYLDGNGQTLV-PKELSNYKHLITLIDLSNNRIISTLSNQSNNQTQL 800
QY      243  BLHLDNKLTTRVP---GGLAEHKYIQVVYIHHNNNISVYGSSDFCPGHNATKKAISGVIS 298
Db      801  TLISYNLRICRIPPTFDGL---KSLRIILSIHGNDISVY-----PEGAFNDISALSILA 851
QY      299  LFSNPV-----QYMIQOSTPFC 316
Db      852  IGANPLCYCDNNQMWLSDWVKSEYK--PGIATC 882

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RESULT 30
US-09-540-245A-2
; Sequence 2, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1525
; TYPE: PRT
; ORGANISM: human
US-09-540-245A-2

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Query Match	18.5%	Score 317	DB 3	Length 1525
Best Local Similarity	25.7%	Pred. No. 1.3e-21		
Matches 101; Conservative	60	Mismatches 120	Indels 112	Gaps 11

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QY      24 CFFRCQHVRVQCSDGLGDKVPKDLPRPTTLIDLONKKITEK-DGDFFNKLKNLAIL 82
           ||::||::||::||::||::||::||::||::||::||::||::||::||::|
Db      502 CEPKRCCEGTVDSCNQKLNKIPEHIFQYTAELRLNNNEFTVLAEATGIFPKLPQLRKINF 561
           ||::||::||::||::||::||::||::||::||::||::||::||::||::|
QY      83 VANKISKYSPPGFPLVKLERLYLSNQOLKELEPKKPRTLQELRA----- 127
           ||::||::||::||::||::||::||::||::||::||::||::||::||::|
Db      562 SNKKITDIEGAFFEGASGVNEILLNSRLENVOHQKFKGLESKLTMLRSNRITYCGNDS 621
           ||::||::||::||::||::||::||::||::||::||::||::||::||::|
QY      128 -----HEMBITKRKYTRGNLMIVIELGNP----- 155
           ||::||::||::||::||::||::||::||::||::||::||::||::||::|
Db      622 FGLGSVRLSLSYDNQITTVAPGAFPTLLSTLNTLANPFNCYLA MWLGWILRRKRIV 681
           ||::||::||::||::||::||::||::||::||::||::||::||::||::|
QY      156 -----LKSGIENGAFQ-----GMKKS-----YIRIDTNI 182
           ||||::||::||::||::||::||::||::||::||::||::||::||::||::|
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Db      682  TGNPRCQKPYFLKELPIQDVAIQDFICDGDNDNSCSPLSRCTECTCLDVTYRGSKNGL 741
QY      183  TSIPOGLPSSLTELHLDGKIKSRVDAASIKGLNLTAKLGISFNSIAVDNGSLANTPHLR 242
       742  KLPKGIPIRDIYELIDGNOQFLTV-PKELSNYKHLTLIDLSNNRKISTLLENQSFNSMTOLL 800
Db      243  ELHLNNNKLTRP---GGIAEHKXYIQVYYLHNNNLSVYGGSSDFCPGHNITKKAISGVS 298
       801  TLTLSYNNRLRCIPRPTFDGL---KSLRLSLISLGNDSIVV-----PEGAFNDISALSHLA 851
QY      299  LFSNPV-----QWYLEIQPSTFRC 316
Db      852  IGANPLYCDGNMOWLSDWKSEYKE-PGIRARC 882

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Search completed: February 9, 2004, 11:39:48
Job time : 32 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2004, 09:24:09 ; Search time 24 Seconds

(without alignments)
644.658 Million cell updates/sec

Title: US-10-004-176-6

Perfect score: 1713
Sequence: 1 VEASGIGPEVDDRDPEPSTL.....QPSTFCVYASAIQIGNYK 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	1709	99.8	359	1	PGS2_HUMAN
2	1587.5	92.7	360	1	P07585 homo sapien
3	1584.5	92.5	360	1	Q29393 canis famil
4	1575.5	92.0	360	1	Q46542 equus cabal
5	1564.5	91.3	360	1	PGS2_PIG
6	1564.5	91.3	360	1	PGS2_BOVIN
7	1562.5	91.2	360	1	PGS2_PABIT
8	1415	82.6	357	1	PGS2_SHEEP
9	1403	81.9	356	1	PGS2_CHICK
10	1365.5	79.7	354	1	PGS2_COTUA
11	1331.5	77.7	354	1	PGS2_MOUSE
12	1022	59.7	368	1	PGS1_RAT
13	985.5	57.5	369	1	PGS1_XENLA
14	984.5	57.5	369	1	PGS1_RAT
15	983.5	57.4	372	1	PGS1_MOUSE
16	982.5	57.4	369	1	PGS1_HORSE
17	979	57.2	368	1	PGS1_SHEEP
18	975.5	56.9	369	1	PGS1_BOVIN
19	972.5	56.8	369	1	PGS1_BOVIN
20	943.5	55.1	379	1	PGS1_CANFA
21	925.5	54.0	373	1	ASPN_HUMAN
22	616	36.0	372	1	ASPN_MOUSE
23	403.5	23.6	377	1	PGS1_PIG
24	402.5	23.5	381	1	PRIP_RAT
25	389	22.7	699	1	PRIP_BOVIN
26	386.5	22.6	378	1	ECM2_HUMAN
27	385.5	22.5	382	1	PRIP_MOUSE
28	381	22.2	135	1	PRIP_HUMAN
29	367.5	21.5	343	1	PGS1_RABIT
30	365.5	21.3	338	1	LUM_COTUA
31	365.5	21.3	343	1	LUM_HUMAN
32	356.5	20.8	342	1	LUM_CHICK
33	353.5	20.6	338	1	LUM_BOVIN
					LUM_MOUSE

34	347.5	20.3	338	1	LUM_RAT
35	342	20.0	649	1	PLR3_HUMAN
36	332	19.4	646	1	PLR1_HUMAN
37	327	19.1	1504	1	SILT_DROME
38	325.5	19.0	352	1	KERA_HUMAN
39	322.5	18.8	376	1	FMOD_HUMAN
40	319.5	18.7	951	1	LG84_HUMAN
41	317.5	18.5	352	1	KERA_BOVIN
42	316	18.4	353	1	KERA_CHICK
43	315	18.4	353	1	KERA_COTUA
44	314.5	18.4	375	1	KERA_BOVIN
45	313.5	18.3	951	1	LG84_RAT

RESULT 1
PGS2_HUMAN STANDARD; PRT; 359 AA.
ID PGS2_HUMAN
AC P07585; Q9P020; Q9P021; Q9Y5N8; Q9Y5N9;
DT 01-APR-1988 (Rel. 07, last sequence update)
DT 01-APR-1988 (Rel. 07, last sequence update)
DT 15-SEP-2003 (Rel. 42, last annotation update)
DE Decorin precursor (Bone proteoglycan II) (PG-S2) (PG40).
GN DCN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=87017013; PubMed=3484330;
RX Krusius T., Ruostelampi E.;
RT "Primary structure of an extracellular matrix proteoglycan core
RT protein deduced from cloned cDNA."
RL Proc. Natl. Acad. Sci. U.S.A. 83:7683-7687(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=93162643; PubMed=8432527;
RA Vetter U., Vogel W., Just W., Young M.F., Fisher L.W.;
RT "Human decorin gene: intron-exon junctions and chromosomal
RT localization."
RL Genomics 15:161-168(1993).
RN [3]
RP SEQUENCE OF 1-70 FROM N.A.
RX MEDLINE=93162642; PubMed=8432526;
RA Danielson K.G., Fazio A., Cohen I.R., Camizzone L., Iozzo R.V.;
RT "The human decorin gene: intron-exon organization, discovery of two
RT alternatively spliced exons in the 5' untranslated region, and
RT mapping of the gene to chromosome 12q23."
RL Genomics 15:146-160(1993).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS A; B; C; D AND E).
RC Se-Szabo G., Glant T.T.;
RT "Alternative splicing of human decorin."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANT MET-268.
RX Rieder M.J., Armet T.Z., Garington D.P., Chung M.-W., Lee K.L.,
RA Ozuna M., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkin R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Martina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley D.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Raley J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywnicki M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [7]
 RP SEQUENCE OF 31-50.
 RX MEDLINE=90073579; PubMed=2590169;
 RA Roughley P.J., White R.J.;
 RT "Dermatan sulphate proteoglycans of human articular cartilage. The
 RT properties of dermatan sulphate proteoglycans I and II.";
 RL Biochem. J. 262:823-827 (1989).
 [8]
 RP SEQUENCE OF 31-49.
 RX MEDLINE=87250639; PubMed=3597437;
 RA Fisher L.W., Hawkins G.R., Turos N., Termine J.D.;
 RT "Purification and partial characterization of small proteoglycans I
 RT and II, bone sialoproteins I and II, and osteonectin from the mineral
 RT compartment of developing human bone.";
 RL J. Biol. Chem. 262:9702-9708 (1987).
 CC -I- FUNCTION: May affect the rate of fibrils formation.
 CC -I- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
 CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
 CC similarity).
 CC -I- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -I- ALTERNATIVE PRODUCTS: Named isoforms=5;
 CC Event=Alternative splicing;
 CC Name=A;
 CC IsoId=P07585-1; Sequence=Displayed;
 CC Name=B;
 CC IsoId=P07585-2; Sequence=VSP_006172;
 CC Name=C;
 CC IsoId=P07585-3; Sequence=VSP_006173;
 CC Name=D;
 CC IsoId=P07585-4; Sequence=VSP_006174;
 CC Name=E;
 CC IsoId=P07585-5; Sequence=VSP_006175, VSP_006176;
 CC -I- PTM: The attached glycosaminoglycan chain can be either
 CC chondroitin sulfate or dermatan sulfate depending upon the tissue
 CC of origin.
 CC -I- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SLRP)
 CC FAMILY. CLASS I SUBFAMILY.
 CC -I- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL; M14219; AAB00774.1; -;
 CC DR EMBL; M1131; AAS52301.1; ALT SEQ.
 CC DR EMBL; L01125; AAS52301.1; JOINED.
 CC DR EMBL; L01126; AAS52301.1; JOINED.
 CC DR EMBL; L01127; AAS52301.1; JOINED.
 CC DR EMBL; L01129; AAS52301.1; JOINED.
 CC DR EMBL; L01130; AAS52301.1; JOINED.
 CC DR EMBL; M98262; AAB60901.1; -;
 CC DR EMBL; AF138300; AAD44713.1; -;
 CC DR EMBL; AF138301; AAF61437.1; -;
 CC DR EMBL; AF138302; AAD44714.1; -;
 CC DR EMBL; AF138303; AAF61438.1; -;

DR EMBL; AF138304; AAD44715.1; -;
 DR EMBL; AF491944; AAL92176.1; -;
 DR EMBL; BC005332; AAH05322.1; -;
 DR PIR; A45016; NEBHC8.
 DR Genew; HENC:2705; DCN.
 DR MIM; 125255; -;
 DR GO; GO:0007397; P.histogenesis and organogenesis; TAS.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000372; LRR_Nterm.
 DR InterPro; IPR003591; LRR_Typ.
 DR Pfam; PF00560; LRR; 8.
 DR Pfam; PF01462; LRRNT; 1.
 DR SMART; SM00369; LRR_Typ; 1.
 DR SMART; SM00013; LRRNT; 1.
 KM Glycoprotein; Extracellular matrix; Repeat;
 KM Leucine-rich repeat; Signal; Alternative splicing; Polymorphism.
 FT SIGNAL 1 16
 FT PROPEP 17 30
 FT CHAIN 31 359
 FT DOMAIN 54 67
 FT REPEAT 73 93
 FT REPEAT 94 117
 FT REPEAT 118 141
 FT REPEAT 142 162
 FT REPEAT 163 186
 FT REPEAT 187 212
 FT REPEAT 213 233
 FT REPEAT 234 257
 FT REPEAT 258 281
 FT REPEAT 282 304
 FT REPEAT 305 334
 FT REPEAT 335 359
 FT DISULFID 54 67
 FT CARBOHYD 313 346
 FT CARBOHYD 34 34
 FT CARBOHYD 211 211
 FT CARBOHYD 262 262
 FT CARBOHYD 303 303
 FT VARSPLIC 71 179
 FT VARSPLIC 73 219
 FT VARSPLIC 109 295
 FT VARSPLIC 72 75
 FT VARSPLIC 76 359
 FT VARIANT 268 268
 FT VARIANT 273 273
 FT CONFLICT 37 37
 FT CONFLICT 45 45
 SQ SEQUENCE 359 AA; 39746 MW; FFE11E871A1A52DD CRC64;
 Query Match 99.8%; Score 1709; DB 1; Length 359;
 Best Local Similarity 100.0%; Pred. No. 8.3e-114; Indels 0; Gaps 0;
 Matches 328; Conservative 0; Mismatches 0;
 QY 2 BASGIGPEVPPDRDEPELGPVCPRCOCHLRVVOCSPLGLDKVKKDLPPTTLTLDLQNN 61
 DB |||||
 QY 32 BASGIGPEVPPDRDEPELGPVCPRCOCHLRVVOCSPLGLDKVKKDLPPTTLTLDLQNN 91
 QY 62 KITEIKDGFKNLKNLHLLIVNNKISVSPGAFPLVYKRLYLKSKQQLKELPERKMT 121
 DB |||||
 QY 92 KITEIKDGFKNLKNLHLLIVNNKISVSPGAFPLVYKRLYLKSKQQLKELPERKMT 151
 QY 122 LOELRAHNEITTKYKRTFNGNLQMTIVLEGTNPKKSGINGNGAQQKKLSYTIATDN 181
 DB |||||
 QY 152 LOELRAHNEITTKYKRTFNGNLQMTIVLEGTNPKKSGINGNGAQQKKLSYTIATDN 211
 DB |||||
 QY 182 ITSIPOGLPSTLTLHDGNKISRVDASLGLNNLAKLGLSPNSISAVDNGSLANTPHL 241

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Db 212 ITSIPQGLPPSLTEHLTDGNKISRVDASLKGANLAKLGISFNSISAVDNGSLANTPHL 271
Qy 242 RELHLDNNKLTVPVPGGLAEHKYIOVYLLNNNISVVGSSDPPPHNTKASYSVSVLS 301
Db 272 RELHLDNNKLTVPVPGGLAEHKYIOVYLLNNNISVVGSSDPPPHNTKASYSVSVLS 331
Qy 302 NPVOYWEIOPSTFRVCYVRSATQLGNYK 329
Db 332 NPVOYWEIOPSTFRVCYVRSATQLGNYK 359

RESULT 2
PGS2 CANFA STANDARD; PRT; 360 AA.
AC 029353;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Decarin precursor (Bone proteoglycan II) (PG-S2).
GN DCMN OR DCMNC.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_Taxid=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Glant T.T.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 244-259 FROM N.A.
RA Venta P.J., Brouillette J.A., Yuzbasliyan-Gurkan V., Brewer G.J.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: May affect the rate of fibrils formation (By similarity).
CC -1- SUBUNIT: Binds to type I and type II collagen, to fibronectin and TGF-beta. Forms a ternary complex with MFAP2 and ELN (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By similarity).
CC -1- PTM: The attached glycosaminoglycan chain can be either chondroitin sulfate or dermatan sulfate depending upon the tissue of origin (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SLRP) FAMILY. CLASS I SUBFAMILY.
CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
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CC -----
DR EMBL; U83141; AAB51245.1; -
DR EMBL; L77684; AAB58062.1; -
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Mterm.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00560; LRR; 8.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00369; LRR_Typ; 1.
DR SMART; SM00013; LRRNT; 1.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat; Leucine-rich repeat; Signal.
FT SIGNAL 1 16
FT PROPEP 17 30
FT CHAIN 31 360
FT DOMAIN 55 94
FT REPEAT 74 98
FT REPEAT 95 118
FT REPEAT 119 142
FT REPEAT 119 142

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FT REPEAT 143 163 LRR-S 2.
FT REPEAT 164 187 LRR-T 3.
FT REPEAT 188 213 LRR-T 4.
FT REPEAT 214 234 LRR-S 3.
FT REPEAT 235 258 LRR-T 5.
FT REPEAT 259 282 LRR-T 6.
FT REPEAT 283 305 LRR-S 4.
FT REPEAT 306 335 LRR-T 7.
FT REPEAT 336 360 LRR-T 8.
FT DISULFID 55 68 BY SIMILARITY.
FT DISULFID 314 347 BY SIMILARITY.
FT CARBOHYD 34 34 O-LINKED (GLYCOSAMINOGLYCAN) (BY SIMILARITY).
FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 360 AA; 39980 MW; 99BE81A9C812906 CRC64;

Query Match 92.7%; Score 1587.5; DB 1; Length 360;
Best Local Similarity 92.4%; Pred. No. 3.3e-105;
Matches 305; Conservative 11; Mismatches 11; Indels 3; Gaps 2;

Qy 2 EASGIGPE--VPDDRDEPSPISGYPVCPQCCHLRVVOQSDGLDKVPKDLPPDTLLDQ 59
Db 32 EASGIGPEADRAVDMPDLE-ILGVPVCPQCCHLRVVOQSDGLDKVPKDLPPDTLLDQ 90
Qy 60 NNKITEIKDGFPKNLKNTLHLLVNNKISKVSPGAFIPVYKLESLYKSKQDLKELPEKMP 119
Db 91 NNKITEIKDGFPKNLKNTLHLLVNNKISKVSPGAFIPVYKLESLYKSKQDLKELPEKMP 150
Qy 120 KTLQELRAHEHETIKRVKVTENGANOMIVIEGTNPVKSSEIENGAFQMKKGLSYRIAD 179
Db 151 KTLQELRAHEHETIKRVKAVNGANOMIVIEGTNPVKSSEIENGAFQMKKGLSYRIAD 210
Qy 180 TMTSIPQGLPPSLTEHLTDGNKISRVDASLKGANLAKLGISFNSISAVDNGSLANTP 239
Db 211 TMTSIPQGLPPSLTEHLTDGNKISRVDASLKGANLAKLGISFNSISAVDNGSLANTP 270
Qy 240 HIREHLHDNNKLTVPVPGGLAEHKYIOVYLLNNNISVVGSSDPPPHNTKASYSVSVLS 299
Db 271 HIREHLHDNNKLTVPVPGGLAEHKYIOVYLLNNNISVVGSSDPPPHNTKASYSVSVLS 330
Qy 300 FSNPVOYWEIOPSTFRVCYVRSATQLGNYK 329
Db 331 FSNPVOYWEIOPSTFRVCYVRSATQLGNYK 360

RESULT 3
PGS2 HORSE STANDARD; PRT; 360 AA.
AC 046542;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Decarin precursor (Bone proteoglycan II) (PG-S2) (Dermatan sulfate proteoglycan II) (DS-PGII).
GN DCMN.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_Taxid=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Richardson D.W., Dodge G.R.;
RL "Effects of interleukin-1 beta and tumor necrosis factor-alpha on the expression of matrix related genes in cultured equine articular chondrocytes."
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP FUNCTION: May affect the rate of fibrils formation (By similarity).
RN [3]
RP SUBUNIT: Binds to type I and type II collagen, to fibronectin and TGF-beta. Forms a ternary complex with MFAP2 and ELN (By similarity).

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CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC similarity).
CC -1- PTM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC (SLRP) FAMILY. CLASS I SUBFAMILY.
CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, AF038127, AAB92652.1, -.
DR InterPro, IPR001611, LRR.
DR InterPro, IPR003372, LRR_Nterm.
DR InterPro, IPR003591, LRR_Cyp.
DR Pfam, PF00560, LRR, 8.
DR Pfam, PF01462, LRRNT, 1.
DR SMART, SM00013, LRRNT, 1.
DR Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
DR Leucine-rich repeat; Signal.
FT SIGNAL 1 16
FT PROPEP 17 30
FT CHAIN 31 360
FT DOMAIN 55 68
FT REPEAT 74 94
FT REPEAT 95 118
FT REPEAT 119 142
FT REPEAT 143 163
FT REPEAT 164 187
FT REPEAT 188 213
FT REPEAT 214 234
FT REPEAT 235 258
FT REPEAT 259 282
FT REPEAT 283 305
FT REPEAT 306 335
FT REPEAT 336 360
FT DISULFID 55 68
FT DISULFID 314 347
FT CARBOHYD 34 34
FT CARBOHYD 190 190
FT CARBOHYD 212 212
FT CARBOHYD 263 263
FT CARBOHYD 304 304
SQ SEQUENCE 360 AA; 39939 MW; 2DAE97DE16F7C45 CR664;

Query Match 92.5%; Score 1584.5; DB 1; Length 360;
Best Local Similarity 92.1%; Pred. No. 5.4e-105;
Matches 304; Conservative 12; Mismatches 11; Indels 3; Gaps 2;

QY 2 BASGIGPE--VPDDDFEPLSGVCPFRQCHLRVVGQSDGLDVKPKDLPDPTLLDQ 59
DB 32 BASGIGPEPRIRHEVLDLP-LGPVCPFRQCHLRVVGQSDGLDVKPKDLPDPTLLDQ 90
QY 60 NKKITEIKGDFPKNLKNTLILVNNKISKVSPGAFPLVKKLELYLSFNOQKEPEKKP 119
DB 91 NKKITEIKGDFPKNLKNTLILVNNKISKVSPGAFPLVKKLELYLSFNOQKEPEKKP 150
QY 120 KTLQSLRAHENEITTKRKVTENGLOMIVIELGTPNPKSSGIENGAFQGMKLSYRIAD 179
DB 151 KTLQSLRAHENEITTKRKAVFENGLOMIVIELGTPNPKSSGIENGAFQGMKLSYRIAD 210
QY 180 TWTSTPQSLPSTLHLDGKISRVDAAASKGNLNAKGLDLSNLSISAVNGSLAMP 239
DB 211 TWTSTPQSLPSTLHLDGKISRVDAAASKGNLNAKGLDLSNLSISAVNGSLAMP 270

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QY 240 HIREHLDDNNKLTFRVPGGLABHKYIQVYVYLNHNNSIVGSSDFCPGHNTKKASYGVL 299
DB 271 HIREHLDDNNKLTFRVPGGLADHKYIQVYVYLNHNNSISAVGSDNFCFPGYNTKASISGVL 330
QY 300 FSNPVOYWEIOPSTFRCYVRSALQGNVK 329
DB 331 FSNPVOYWEIOPSTFRCYVRSALQGNVK 360

RESULT 4
PGS2 FIG STANDARD; PRT; 360 AA.
AC Q9XSD9; Q9XSH4;
ID 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Decorin precursor (Bone proteoglycan II) (Pg-S2).
GN DCN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN (1)
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC STRAIN=Yorkshire;
RA Stephenson S., Schnoke M., Vesely I.;
RT "Cloning of the porcine decorin gene.";
RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: May affect the rate of fibrils formation (By
CC similarity).
CC -1- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -1- SURCELLULAR LOCATION: Secreted; extracellular matrix.
CC -1- ALTERNATIVE PRODUCTS:
CC Name=Long;
CC IsoId=Q9XSD9-1; Sequence=Displayed.
CC Name=Short;
CC IsoId=Q9XSD9-2; Sequence=VSP 006177;
CC -1- PTM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SLRP)
CC FAMILY. CLASS I SUBFAMILY.
CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, AF125537, AAD33578.1, -.
DR EMBL, AF140270, AAD33862.1, -.
DR InterPro, IPR001611, LRR.
DR InterPro, IPR003372, LRR_Nterm.
DR InterPro, IPR003591, LRR_Cyp.
DR Pfam, PF00560, LRR, 8.
DR Pfam, PF01462, LRRNT, 1.
DR SMART, SM00369, LRR, 2.
DR SMART, SM00013, LRRNT, 1.
DR Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
DR Leucine-rich repeat; Signal; Alternative splicing.
FT SIGNAL 1 16

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FT PROPEP 17. 30 BY SIMILARITY.
 FT CHAIN 31 360 DECORIN.
 FT DOMAIN 55 68 CYS-RICH.
 FT REPEAT 74 94 LRR-S 1.
 FT REPEAT 95 118 LRR-T 1.
 FT REPEAT 119 142 LRR-T 2.
 FT REPEAT 143 163 LRR-S 2.
 FT REPEAT 164 187 LRR-T 3.
 FT REPEAT 188 213 LRR-T 4.
 FT REPEAT 214 234 LRR-S 3.
 FT REPEAT 235 258 LRR-T 5.
 FT REPEAT 259 282 LRR-T 6.
 FT REPEAT 283 305 LRR-S 4.
 FT REPEAT 306 335 LRR-T 7.
 FT REPEAT 336 360 LRR-T 8.
 FT DISULFID 55 68 BY SIMILARITY.
 FT DISULFID 314 347 O-LINKED (GLYCOSAMINOGLYCAN).
 FT CARBOHYD 34 34 (BY SIMILARITY).
 FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 281 318 Missing (in isoform Short).
 FT SEQUENCE 360 AA; 39899 MW; 8573DEBDBA7509 CRC64;
 SQ
 Query Match 92.0%; Score 1575.5; DB 1; Length 360;
 Best Local Similarity 91.2%; Pred. No. 2.3e-104;
 Matches 301; Conservative 12; Mismatches 14; Indels 3; Gaps 2;

QY 2 EASGIGPE--VPDDDFEBSLGPVCPFCQCHLRVVOGDLGLDVKPKDLPDPTLLDQ 59
 DB 32 EASGIGPERFVEVELEP-LGPMDPFRQCHLRVVOGDLGLDVKPKDLPDPTLLDQ 90
 QY 60 NKKTEIKDGFKNLKNLHALILVNKISKVSPGATPLVKLERLYLSNQLKEPEKAP 119
 DB 91 NKKTEIKDGFKNLKNLHALILVNKISKVSPGATPLVKLERLYLSNQLKEPEKAP 150
 QY 120 KTLQSLRAHENEITKRAKTFNGLNOMLYEITGNPLKSSGJENGAFOGKKLSYRIND 179
 DB 151 KTLQSLRAHENEITKRAKTFNGLNOMLYEITGNPLKSSGJENGAFOGKKLSYRIND 210
 QY 180 TMTISIPQSLPSTLTHLDGNKISVDAASLKGILNLLKLGISFNSISAVNGSLANTP 239
 DB 211 TMTISIPQSLPSTLTHLDGNKISVDAASLKGILNLLKLGISFNSISAVNGSLANTP 270
 QY 240 HURELHLDNNKLTFRVVGGLAEHKYIOVYVLIHNNNISVWSSDFCPGHTTKKASVGSVL 299
 DB 271 HURELHLDNNKLTFRVVGGLAEHKYIOVYVLIHNNNISVWSSDFCPGHTTKKASVGSVL 330
 QY 300 FSNPVOYWEIQPSTFRCVYVRSALQGNKY 329
 DB 331 FSNPVOYWEIQPSTFRCVYVRSALQGNKY 360

RESULT 5
 PGS2 BOVIN
 ID PGS2 BOVIN STANDARD; PRT; 360 AA.
 AC P21793;
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DB Decorin precursor (Bone proteoglycan II) (Pg-S2).
 GN DCN.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OK NCBI_TaxId=9913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88133946; PubMed=3435485;
 RA Day A.A., McQuillan C.I., Termine J.D., Young M.R.;

RT "Molecular cloning and sequence analysis of the cDNA for small
 RT proteoglycan II of bovine bone."
 RL Biochem. J. 248:801-805(1987).
 RN [2]
 RP SEQUENCE OF 31-54.
 RX MEDLINE=89123388; PubMed=2914936;
 RA Choi H.U., Johnson T.L., Pal S., Tang L.H., Rosenberg L.C.,
 RA Neame P.J.;
 RT "Characterization of the dermatan sulfate proteoglycans, DS-PGI and
 RT DS-PGII, from bovine articular cartilage and skin isolated by octyl-
 RT sepharose chromatography."
 RL J. Biol. Chem. 264:2876-2884(1989).
 RN [3]
 RP INTERACTION WITH MPA2 AND ELN.
 RX MEDLINE=21683536; PubMed=11721332.
 RA Reinboch B., Hanssen E., Cleary E.G., Gibson M.A.;
 RT "Molecular interactions of biglycan and decorin with elastic fiber
 RT components: biglycan forms a ternary complex with tropoelastin and
 RT microfibril-associated glycoprotein 1."
 RL J. Biol. Chem. 277:3950-3957(2002).
 CC -1- FUNCTION: May affect the rate of fibrils formation.
 CC -1- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
 CC TGF-beta. Forms a ternary complex with MPA2 and ELN.
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -1- PTM: The attached glycosaminoglycan chain can be either
 CC chondroitin sulfate or dermatan sulfate depending upon the tissue
 CC of origin.
 CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
 CC (SLRP) FAMILY. CLASS I SUBFAMILY.
 CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: Y00712; CAA68702.1; -.
 CC PIR: S06280; S06280.
 CC InterPro: IPR001611; LRR.
 CC InterPro: IPR00372; LRR_Nterm.
 CC InterPro: IPR003591; LRR_Typ.
 CC Pfam: PF00560; LRR; 9.
 CC Pfam: PF01462; LRRNT; 1.
 CC SMART: SM00369; LRR_Typ; 2.
 CC SMART: SM00013; LRRNT; 1.
 CC Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 CC Leucine-rich repeat; Signal.
 CC SIGNAL 1 16
 FT PROPEP 17 30
 FT CHAIN 31 360
 FT DOMAIN 55 68
 FT REPEAT 74 94
 FT REPEAT 95 118
 FT REPEAT 119 142
 FT REPEAT 143 163
 FT REPEAT 164 187
 FT REPEAT 188 213
 FT REPEAT 214 234
 FT REPEAT 235 258
 FT REPEAT 259 282
 FT REPEAT 283 305
 FT REPEAT 306 335
 FT REPEAT 336 360
 FT DISULFID 55 68
 FT DISULFID 314 347
 FT CARBOHYD 34 34
 FT CARBOHYD 212 212
 FT CARBOHYD 263 263
 FT CARBOHYD 304 304

DECORIN.
 CYS-RICH.
 LRR-S 1.
 LRR-T 1.
 LRR-T 2.
 LRR-S 2.
 LRR-T 3.
 LRR-T 4.
 LRR-S 3.
 LRR-T 5.
 LRR-T 6.
 LRR-S 4.
 LRR-T 7.
 LRR-T 8.
 BY SIMILARITY.
 O-LINKED (GLYCOSAMINOGLYCAN) (BY
 SIMILARITY).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 360 AA; 39837 MW; 71E84DA2D87552C0 CRC64;
 Query Match 91.3%; Score 1564.5; DB 1; Length 360;
 Best Local Similarity 89.7%; Pred. No. 1,4e-103;
 Matches 296; Conservative 19; Mismatches 12; Indels 3; Gaps 2;
 QY 2 EASGIGPE--VPDRDFEPLSGVCPFCQCHLRVQCSDLGIDKVPKDLPPDTLLDQ 59
 DB 32 EASGIGPEEHPPEPEEP-MGVPCEPRCQCHLRVQCSDLGIDKVPKDLPPDTLLDQ 90
 QY 60 NNKITEIKDGFKNLKNLHALILVNNKISKVSPGAFPTLVKLERLYLSNOKLEPEKXP 119
 DB 91 NNKITEIKDGFKNLKNLHALILVNNKISKVSPGAFPTLVKLERLYLSNOKLEPEKXP 150
 QY 120 KTLQELRAHENEITTKRKVTENGKQMTVEIGTNPVLSGSIENGAFQMKLSYRIAD 179
 DB 151 KTLQELRAHENEITTKRKVSFNGLNQMTVEIGTNPVLSGSIENGAFQMKLSYRIAD 210
 QY 180 TMTSTIPOGLPESLTELHDGKISRVDASLKGNNLAKLGISFNSISAVNGSLANTP 239
 DB 211 TMTSTIPOGLPESLTELHDGKISRVDASLKGNNLAKLGISFNSISAVNGSLANTP 270
 QY 240 HURELHDNNKLTREVPGLAEHKYIQVYVLAHNNNISVVGSSDPCPGHNTKASYSVSL 299
 DB 271 HURELHDNNKLTREVPGLAEHKYIQVYVLAHNNNISVVGSSDPCPGHNTKASYSVSL 330
 QY 300 FSNPVOYWEIOPSTFCVYVRSALIOLGNYK 329
 DB 331 FSNPVOYWEIOPSTFCVYVRSALIOLGNYK 360
 RESULT 6
 PG82_RABIT STANDARD; PRT; 360 AA.
 ID Q28888; Q28888; (Rel. 38, Created)
 AC 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Decorin precursor (Bone proteoglycan II) (PG-S2).
 GN DCN.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OK NCBI_TaxID=9986;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cornea;
 RX MEDLINE=9512319; PubMed=7822148;
 RA Zhan Q., Burrows R., Clinton C.;
 RT "Cloning and in situ hybridization of rabbit decorin in corneal
 tissues";
 RL Invest. Ophthalmol. Vis. Sci. 36:206-215 (1995).
 RN (2)
 RP SEQUENCE OF 38-358 FROM N.A.
 RC TISSUE=Cartilage;
 RA Hering T.M., Kollar J.;
 RT "The primary structure of rabbit chondrocyte decorin deduced from
 nucleotide sequence";
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: May affect the rate of fibrils formation (By
 similarity).
 CC -1- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
 TGF-beta. Forms a ternary complex with MFAP2 and ELM (By
 similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
 similarity).
 CC -1- PTM: The attached glycosaminoglycan chain can be either
 chondroitin sulfate or dermatan sulfate depending upon the tissue
 of origin (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
 (SLRP) FAMILY. CLASS I SUBFAMILY.
 CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.

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 CC -----
 DR EMBL; 576584; AAB33083.1; -
 DR EMBL; U03394; AAC04315.1; -
 DR PIR; I47020; I47020.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR003712; LRR_Nterm.
 DR InterPro; IPR003591; LRR_Typ.
 DR Pfam; PF00560; LRR; 8.
 DR Pfam; PF01462; LRRNT; 1.
 DR SMART; SM00369; LRR_Typ; 1.
 DR SMART; SM00013; LRRNT; 1.
 KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 KW Leucine-rich repeat; Signal.
 FT SIGNAL 1 16
 FT PROPEP 17 30
 FT CHAIN 31 360
 FT DOMAIN 55 68
 FT REPEAT 74 94
 FT REPEAT 95 118
 FT REPEAT 119 142
 FT REPEAT 143 163
 FT REPEAT 164 187
 FT REPEAT 188 213
 FT REPEAT 214 234
 FT REPEAT 235 258
 FT REPEAT 259 282
 FT REPEAT 283 305
 FT REPEAT 306 335
 FT REPEAT 336 360
 FT DISULFID 347
 FT DISULFID 347
 FT CARBOHYD 34 34
 FT CARBOHYD 212 212
 FT CARBOHYD 263 263
 FT CARBOHYD 304 304
 SQ SEQUENCE 360 AA; 39896 MW; 0B50C6756FE02369 CRC64;
 Query Match 91.3%; Score 1564.5; DB 1; Length 360;
 Best Local Similarity 90.6%; Pred. No. 1,4e-103;
 Matches 299; Conservative 17; Mismatches 11; Indels 3; Gaps 2;
 QY 2 EASGIGPE--VPDRDFEPLSGVCPFCQCHLRVQCSDLGIDKVPKDLPPDTLLDQ 59
 DB 32 EASGIGPEEHPPEPEEP-MGVPCEPRCQCHLRVQCSDLGIDKVPKDLPPDTLLDQ 90
 QY 60 NNKITEIKDGFKNLKNLHALILVNNKISKVSPGAFPTLVKLERLYLSNOKLEPEKXP 119
 DB 91 NNKITEIKDGFKNLKNLHALILVNNKISKVSPGAFPTLVKLERLYLSNOKLEPEKXP 150
 QY 120 KTLQELRAHENEITTKRKVTENGKQMTVEIGTNPVLSGSIENGAFQMKLSYRIAD 179
 DB 151 KTLQELRAHENEITTKRKVSFNGLNQMTVEIGTNPVLSGSIENGAFQMKLSYRIAD 210
 QY 180 TMTSTIPOGLPESLTELHDGKISRVDASLKGNNLAKLGISFNSISAVNGSLANTP 239
 DB 211 TMTSTIPOGLPESLTELHDGKISRVDASLKGNNLAKLGISFNSISAVNGSLANTP 270
 QY 240 HURELHDNNKLTREVPGLAEHKYIQVYVLAHNNNISVVGSSDPCPGHNTKASYSVSL 299
 DB 271 HURELHDNNKLTREVPGLAEHKYIQVYVLAHNNNISVVGANDPCPGHNTKASYSVSL 330
 QY 300 FSNPVOYWEIOPSTFCVYVRSALIOLGNYK 329
 DB 331 FSNPVOYWEIOPSTFCVYVRSALIOLGNYK 360

RESULT 7
PGS2 SHEEP STANDARD; PRT; 360 AA.
AC PGS2 SHEEP
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Decorin precursor (Bone proteoglycan II) (PG-S2) (PG40).
GN DCN.
OS Ovis aries (Sheep).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_Taxid=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Myometrium;
RX MEDLINE=20113292; PubMed=10644528;
RA Wu W.X., Zhang Q., Uno N., Dicks J.B., Nathanielsz P.W.;
RT "Characterization of decorin mRNA in pregnant intrauterine tissues of
RL Am. J. Physiol. 278:C199-C206(2000)."
CC -1- FUNCTION: May affect the rate of fibrils formation (By
CC similarity).
CC -1- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC similarity).
CC -1- PTM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC (SLRP) FAMILY. CLASS I SUBFAMILY.
CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AF125041; AAF00585.1; -.
DR HSSP; P09661; IAGN.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00560; LRR; 9.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00369; LRR_Typ; 2.
DR SMART; SM00013; LRRNT; 1.
KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT SIGNAL 1 16
FT PROPEP 17 30
FT CHAIN 31 360
FT DOMAIN 55 68
FT REPEAT 74 94 LRR-S 1.
FT REPEAT 95 118 LRR-T 1.
FT REPEAT 119 142 LRR-T 2.
FT REPEAT 143 163 LRR-S 2.
FT REPEAT 164 187 LRR-T 3.
FT REPEAT 188 213 LRR-T 4.
FT REPEAT 214 234 LRR-S 3.
FT REPEAT 235 258 LRR-T 5.
FT REPEAT 259 282 LRR-T 6.
FT REPEAT 283 305 LRR-S 4.
FT REPEAT 306 335 LRR-T 7.
FT REPEAT 336 360 LRR-T 8.
FT DISULFID 55 68
FT BY SIMILARITY.

FT DISULFID 314 347 BY SIMILARITY.
FT CARBOHYD 34 34 O-LINKED (GLYCOSAMINOGLYCAN) (BY
FT SIMILARITY).
FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 360 AA; 39972 MW; 0095D0DFDA88624 CRC64;
Query Match 91.2%; Score 1562.5; DB 1; Length 360;
Best Local Similarity 89.5%; Pred. No. 1.9e-103;
Matches 298; Conservative 17; Mismatches 9; Indels 9; Gaps 3;
QY 2 EASGICP-----EVPDDRDFEPSTLGPVCPFCQCHLRVQCSDGLDVKYKDLPPDTLL 56
DB 32 EASGIGPERHFEV---ELBP-MGPVCPFRQCHLRVQCSDGLDVKYKDLPPDTLL 87
QY 57 DIQNNKITEIKDGDENKLNKLNHALLVNKKISKVSPGAFPLVKLERLYLSKNQKEPE 116
DB 88 DIQNNKITEIKDGDENKLNKLNHALLVNKKISKVSPGAFPLVKLERLYLSKNQKEPE 147
QY 117 KKPCKTLOELRAHEKITVYRKTFNGLNOMVIELGTPIPKSSGIENGAFOGKTLSTYR 176
DB 148 KKPCKTLOELRAHEKITVYRKTFNGLNOMVIELGTPIPKSSGIENGAFOGKTLSTYR 207
QY 177 IADNTITSIPGLPSTLTELHDGKISRVDASLKGNNLAKLGLSFNSISAVNGSLA 236
DB 208 IADNTITSIPGLPSTLTELHDGKISRVDASLKGNNLAKLGLSFNSISAVNGSLA 267
QY 237 NTPHLRELHLNKKLTRVPGGLAEHKYIQVYLLHNNNISVYSSDFCPGHNTKASYSG 296
DB 268 NTPHLRELHLNKKLTRVPGGLAEHKYIQVYLLHNNNISVYSSDFCPGHNTKASYSG 327
QY 297 VSLFSPVQVWEIQSTRTCYVYVSAIDGNYK 329
DB 328 VSLFSPVQVWEIQSTRTCYVYVSAIDGNYK 360
RESULT 8
PGS2 CHICK STANDARD; PRT; 357 AA.
AC PGS2 CHICK
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Decorin precursor (Bone proteoglycan II) (PG-S2).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_Taxid=9031;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=White leghorn; TISSUE=Cornea;
RX MEDLINE=92296755; PubMed=1605630;
RA Li W., Vergnes J.-P., Cornet P.K., Hassell J.R.;
RT "cDNA clone to chick corneal chondroitin/dermatan sulfate
RT proteoglycan reveals identity to decorin.";
RL Arch. Biochem. Biophys. 296:190-197(1992)."
CC -1- FUNCTION: May affect the rate of fibrils formation (By
CC similarity).
CC -1- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC TGF-beta. Forms a ternary complex with MFAP2 and ELN (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC similarity).
CC -1- PTM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC (SLRP) FAMILY. CLASS I SUBFAMILY.
CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC -----
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DR EMBL, X63797; CNA45318.1; -
DR PIR; S24317; S24317.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR Nterm.
DR InterPro; IPR003591; LRR typ.
DR Pfam; PR00560; LRR-10.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00369; LRR typ; 2.
DR SMART; SM00013; LRRNT; 1.
KM Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KM Leucine-rich repeat; Signal.
FT SIGNAL 1 16
FT PROPEP 17 30
FT CHAIN 31 357
FT DOMAIN 52 65
FT REPEAT 71 91
FT REPEAT 92 115
FT REPEAT 116 139
FT REPEAT 140 160
FT REPEAT 161 184
FT REPEAT 185 210
FT REPEAT 211 231
FT REPEAT 232 255
FT REPEAT 256 279
FT REPEAT 280 302
FT REPEAT 303 332
FT REPEAT 333 357
FT DISULFID 52 65
FT DISULFID 311 344
FT CARBOHYD 34 344
FT CARBOHYD 209 209
FT CARBOHYD 260 260
SQ SEQUENCE 357 AA; 39687 MW; 31B104C7C3CD711D CRC64;

Query Match 82.6%; Score 1415; DB 1; Length 357;
Best Local Similarity 80.2%; Pred. No. 5.1e-93;
Matches 264; Conservative 28; Mismatches 37; Indels 0; Gaps 0;

QY 1 VEASGIGPEVPDRDREPSIGPYCPRCQCHLAVOCSDLGDKVKDLPPTLLLDLON 60
DB 29 IEDEGSADMAPTDDPVISGFGPCPCQCHLKVOCSDLGLERVKDLPPTLLLDLON 88
QY 61 NKITEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLERLYLKSKQLKELPEKMPK 120
DB 89 NKITEIKEDGFKNLKNLHLLVNNKISKSPAAFPALKLERLYLKSKQLKELPEKMPK 148
QY 121 TLQELRAHENEITKVKKVTNPGLNQMIIVLELGNPKSSGIENGAFQGMKQLSYIRIADT 180
DB 149 SLQETIRAHNEISKLRKAVENGILNQVIVLELGNPKSSGIENGAFQGMKRLSYIRIADT 208
QY 181 NITSIRQGLPPSLTEHLDNKISRVDASIKGLNLAATLGLSPNISAVDNGSLANTH 240
DB 209 NITSIRPKGLPPSLTEHLDNKISKIDAGLSGLNLAATLGLSPNISAVDNGSLNVH 268
QY 241 LRELHLDNNKLTTRVPGLAEHKYIQVYVLLHNNNISVVGSSDPFCPGHNTKASYSVSLF 300
DB 269 LRELHLDNNELVAVPGLGEHKYIQVYVLLHNNKIASIGINDPCLGYNTKATYSVSLF 328
QY 301 SNPVQYWEIQSTPRCVYVRSALQCANRK 329
DB 329 SNPVQYWEIQPSAFCHERSAVQIGNYK 357

ID PG82_COTJA STANDARD; PRT; 356 AA.
AC Q9DE68;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Decorin precursor (Bone proteoglycan II) (PG-S2).
GN DGN.
OS *Coturnix coturnix japonica* (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC *Coturnix*.
OX NCBI_TaxID=93934;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cornea, and Sclera;
RX MEDLINE=20556471; PubMed=1102759;
RA Corpeuz L.M., Dunlevy J.R., Hassell J.R., Conrad A.H., Conrad G.W.;
RT "Molecular cloning and relative tissue expression of decorin and
RT lumican in embryonic quail cornea."
RL Matrix Biol. 19:699-704(2000).
CC -1- FUNCTION: May affect the rate of fibrils formation (By
CC similarity).
CC -1- SUBUNIT: Binds to type I and type II collagen, to fibronectin and
CC TGF-beta. Forms a ternary complex with MPAP2 and ELN (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
CC similarity).
CC -1- PTM: The attached glycosaminoglycan chain can be either
CC chondroitin sulfate or dermatan sulfate depending upon the tissue
CC of origin (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC (SLRP) FAMILY. CLASS I SUBFAMILY.
CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC
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DR EMBL; AF125250; AAG48154.1; -
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR Nterm.
DR InterPro; IPR003591; LRR typ.
DR Pfam; PF00560; LRR; 10.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00369; LRR typ; 2.
KM Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KM Leucine-rich repeat; Signal.
FT SIGNAL 1 15
FT PROPEP 16 29
FT CHAIN 30 356
FT DOMAIN 51 64
FT REPEAT 70 90
FT REPEAT 91 114
FT REPEAT 115 138
FT REPEAT 139 159
FT REPEAT 160 183
FT REPEAT 184 209
FT REPEAT 210 230
FT REPEAT 231 254
FT REPEAT 255 278
FT REPEAT 279 301
FT REPEAT 302 331
FT REPEAT 332 356
FT DISULFID 51 64
FT DISULFID 310 343
FT CARBOHYD 33 33
FT CARBOHYD 208 208

POTENTIAL.
BY SIMILARITY.
DECORIN.
CYS-RICH.
LRR-S 1.
LRR-T 1.
LRR-T 2.
LRR-S 2.
LRR-T 3.
LRR-T 4.
LRR-S 3.
LRR-T 5.
LRR-T 6.
LRR-S 4.
LRR-T 7.
LRR-T 8.
BY SIMILARITY.
O-LINKED (GLYCOSAMINOGLYCAN) (BY
SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 356 AA; 39571 MW; BE9583C6AED7DB26 CRC64;
 Query Match 81.9%; Score 1403; DB 1; Length 356;
 Best Local Similarity 84.1%; Pred. No. 3.6e-92;
 Matches 260; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 21 GVCPCPCCHLAVVQCSDLGDKVYKDPPTTLLDLDONNKITEKODGPKNLKYLAL 80
 DB 48 GVCPCPCCHLAVVQCSDLGDKVYKDPPTTLLDLDONNKITEKODGPKNLKYLAL 107
 QY 81 ILVNNKISVSPGAFPLVLEKRLYLKSNQKLEPKMKETLOELRAHNEITKVKATF 140
 DB 108 ILVNNKISVSPGAFPLVLEKRLYLKSNQKLEPKMKETLOELRAHNEITKVKATF 167
 QY 141 NGLNOMVIELGTNPLKSSGIEGAGQMKKLSYRIADNTITSIGSPSITELHLG 200
 DB 168 NGLNOMVIELGTNPLKSSGIEGAGQMKKLSYRIADNTITSIGSPSITELHLG 227
 QY 201 NKISRVDASLKLNNLAKLGSPNSISAVDNGSLANTPHIRELHNNKLTFRVPGSLAE 260
 DB 228 NKISRVDASLKLNNLAKLGSPNSISAVDNGSLANTPHIRELHNNKLTFRVPGSLAE 287
 QY 261 HKTIQVYVLLHNNNISVVGSSDFPCPGHNTKASYSVSVLPSPVQYWEIOPSTFRCVYR 320
 DB 288 HKTIQVYVLLHNNNISVVGSSDFPCPGHNTKASYSVSVLPSPVQYWEIOPSTFRCVYR 347
 QY 321 SAIQGNKY 329
 DB 348 SAQVIGNYK 356

RESULT 10
 PG52 MOUSE STANDARD; PRT; 354 AA.

ID PG52 MOUSE STANDARD; PRT; 354 AA.
 AC P28654;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Decortin precursor (Bone proteoglycan II) (PG-S2) (PG40).
 GN DCM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NIH Swiss; TISSUE=Fibroblast;
 RA Naitoh Y., Suzuki S.;
 RL Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95050610; Pubmed=7961765;
 RA Scholzen T., Solursh M., Suzuki S., Reiter R., Morgan J.L.,
 RA Buchberg A.M., Stracusa L.D., Iozzo R.V.;
 RT "The murine decortin. Complete cDNA cloning, genomic organization,
 RT chromosomal assignment, and expression during organogenesis and
 RT tissue differentiation.";
 RL J. Biol. Chem. 269:28270-28281(1994).
 CC -1- FUNCTION: May affect the rate of fibrils formation.
 CC -1- SUBUNIT: Bands to type I and type II collagen, to fibronectin and
 CC TGF-beta. Forms a ternary complex with MMP2 and Eln (by
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -1- PTM: The attached glycosaminoglycan chain can be either
 CC chondroitin sulfate or dermatan sulfate depending upon the tissue
 CC of origin (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
 CC (SLRP) FAMILY. CLASS I SUBFAMILY.
 CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
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 CC -----

DR EMBL; X53929; CAA37876.1;
 DR PIR; A55454; A55454.
 DR HSP; P23945; 1XUN.
 DR MGD; MGI:94872; Dcn.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR003712; LRR_Nterm.
 DR InterPro; IPR003591; LRR_Typ.
 DR Pfam; PF00560; LRR; 9.
 DR Pfam; PF01462; LRRNT; 1.
 DR SMART; SM00369; LRR_Typ; 2.
 DR SMART; SM00013; LRRNT; 1.
 KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 KW Leucine-rich repeat; Signal.
 FT SIGNAL 1 16
 FT PROPEP 17 30
 FT CHAIN 31 354
 FT DOMAIN 49 62
 FT REPEAT 68 88
 FT REPEAT 89 112
 FT REPEAT 113 136
 FT REPEAT 137 157
 FT REPEAT 158 181
 FT REPEAT 182 207
 FT REPEAT 208 228
 FT REPEAT 229 252
 FT REPEAT 253 276
 FT REPEAT 277 299
 FT REPEAT 300 329
 FT REPEAT 330 354
 FT DISULFID 49 62
 FT DISULFID 308 341
 FT CARBOHYD 34 34
 FT CARBOHYD 206 206
 FT CARBOHYD 241 241
 FT CARBOHYD 257 257
 FT CARBOHYD 298 298
 SQ SEQUENCE 354 AA; 39809 MW; F05B5CC08CABF6F CRC64;

Query Match 79.7%; Score 1365.5; DB 1; Length 354;
 Best Local Similarity 79.9%; Pred. No. 1.6e-89;
 Matches 262; Conservative 28; Mismatches 33; Indels 5; Gaps 1;

QY 2 BASGIGPEVPPDRDRDEPSLGPVCPFCPCCHLAVVQCSDLGDKVYKDPPTTLLDLDONN 61
 DB 32 BASGIIIPYDPDN-----PLISMCPCPCCHLAVVQCSDLGDKVYKDPPTTLLDLDONN 86
 QY KITEIKDGPDKLKNLHALLVNNKISKVSPGAFPLVLEKRLYLKSNQKLEPKMKET 121
 DB 62 KITEIKDGPDKLKNLHALLVNNKISKVSPGAFPLVLEKRLYLKSNQKLEPKMKET 146
 QY KITEIKDGPDKLKNLHALLVNNKISKVSPGAFPLVLEKRLYLKSNQKLEPKMKET 146
 DB 87 KITEIKDGPDKLKNLHALLVNNKISKVSPGAFPLVLEKRLYLKSNQKLEPKMKET 166
 QY 122 LOELRAHNEITKVKATFENGILNOMVIELGTNPLKSSGIEGAGQMKKLSYRIADNT 181
 DB 147 LOELRAHNEITKVKATFENGILNOMVIELGTNPLKSSGIEGAGQMKKLSYRIADNT 206
 QY 182 ITISIPGCLPSTELHLDNKISRYDASLKLNNLAKLGSPNSISAVDNGSLANTPHL 241
 DB 207 ITAIPGCLPSTELHLDNKITKVDAPLKGILNLSKGLSPNSITVWENGLAVPHL 266
 QY 242 RELHLDNNKLTVPGGLAEHKTIQVYVLLHNNNISVVGSSDFPCPGHNTKASYSVSVLP 301
 DB 267 RELHLDNNKLTVPGGLAEHKTIQVYVLLHNNNISVVGSSDFPCPGHNTKASYSVSVLP 326
 QY 302 NPVQWEIOPSTFRCVYSAIQGNKY 329
 DB 327 NPVQWEIOPSTFRCVYSAIQGNKY 354

RESULT 11
PGS2 RAT STANDARD; PRT; 354 AA.

AC 001139;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Decorin precursor (Bone proteoglycan II) (PG-82) (PG40) (Dermatan sulfate proteoglycan-II) (DSPG).
GN DCM.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Uterus;
RX MEDLINE=93003331; PubMed=1390895;
RA Abramson S.R., Woessner J.F.;
RT "CDNA sequence for rat dermatan sulfate proteoglycan-II (decorin).";
RL Biochim. Biophys. Acta 1132:225-227(1992).
RN [2]
RP SEQUENCE OF 11-354 FROM N.A.
RX MEDLINE=93154359; PubMed=1493796;
RA Aducci V.K., Dreher K.L.;
RT "Molecular characterization of vascular smooth muscle decorin: deduced core protein structure and regulation of gene expression.";
RL Eur. J. Cell Biol. 59:314-321(1992).
RN [3]
RP SEQUENCE OF 31-48 AND 171-191.
RC STRAIN=Sprague-Dawley; TISSUE=Uterus;
RX MEDLINE=89350825; PubMed=2764879;
RA Kokenyesi R., Woessner J.F.;
RT "Purification and characterization of a small dermatan sulfate proteoglycan implicated in the dilatation of the rat uterine cervix.";
RL Biochem. J. 260:413-419(1989).
CC -1- FUNCTION: May affect the rate of fibrils formation (by similarity). May be implicated in the dilatation of the rat cervix.
CC -1- SUBUNIT: Binds to type I and type II collagen, to fibronectin and TGF-beta. Forms a ternary complex with MFAP2 and ELN (by similarity).
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -1- DEVELOPMENTAL STAGE: The amount of DSPG per cervix increases 4-fold during pregnancy, then falls precipitously within 1 day post partum.
CC -1- PTM: The attached glycosaminoglycan chain can be either chondroitin sulfate or dermatan sulfate depending upon the tissue of origin (by similarity).
CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SLRP) FAMILY. CLASS 1 SUBFAMILY.
CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC -----
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CC -----
DR EMBL; Z12296; CAA78170.1; -;
DR EMBL; X59859; CAA42519.1; -;
DR PIR; S29145; S29145.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_typ.
DR Pfam; PF00560; LRR_9.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00369; LRR_typ; 2.
DR SMART; SM00013; LRRNT; 1.

KM Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
KW Leucine-rich repeat; Signal.
FT STGNAL 1 16 POTENTIAL.
FT PROEP 17 30
FT CHAIN 31 354 DECORIN.
FT DOMAIN 49 62 CYS-RICH.
FT REPEAT 68 88 LRR-S 1.
FT REPEAT 89 112 LRR-T 1.
FT REPEAT 113 136 LRR-T 2.
FT REPEAT 137 157 LRR-S 2.
FT REPEAT 158 181 LRR-T 3.
FT REPEAT 182 207 LRR-T 4.
FT REPEAT 208 228 LRR-S 3.
FT REPEAT 229 252 LRR-T 5.
FT REPEAT 253 276 LRR-T 6.
FT REPEAT 277 299 LRR-S 4.
FT REPEAT 300 329 LRR-T 7.
FT REPEAT 330 354 LRR-T 8.
FT DISULFID 49 62
FT DISULFID 308 341
FT CARBOHYD 34 34
FT CARBOHYD 184 184
FT CARBOHYD 206 206
FT CARBOHYD 241 241
FT CARBOHYD 257 257
FT CARBOHYD 298 298
SQ SEQUENCE 354 AA; 39805 MW; 152D92F42D9F5A5B CRC64;
Query Match 77.7%; Score 1331.5; DB 1; Length 354;
Best Local Similarity 77.1%; Pred. No. 4.1e-87;
Matches 233; Conservative 33; Mismatches 37; Indels 5; Gaps 1;
QY 2 BASGISEVDDRDDEPSSSLGVCPCPCQCHLRVQCSDGLDGVDPDPTLLDLQNN 61
DB 32 BASGILPYDPDN-----PLISMCPCVQCCHLRVQCSDGLDGVDPDPTLLDLQNN 86
QY 62 KTEIKDGPDKIKNIAHILVNKISKVSPGAFPLVLERLYLSRNLKEIPKPKT 121
DB 87 KTEIKEGAFKIKDKLHTLILVNKISKISPEAFKVLRLERLYLSKMKELPKLPKT 146
QY 122 LOELRAHEMITVRVTEGNGLNOMVILEGTPKSSGIGENGAFGMKKLSYIRADTV 181
DB 147 LOELRLHDEITLTKSVTEGNGLNMRVILEGTPKNSGIGENGAFGMKGLGIRISDIN 206
QY 182 ITSIPQGLPPLSTELHLDGKISRVDAAALGKLNIAKGLSFNSISAVDNGSIANTPHL 241
DB 207 ITAIPOGLPTISIELHLDGKIAKVDAAALGKNSISKLGSPNSITVVENGLAVPHL 266
QY 242 RELHLDNNKLTTRVPGLAHEKTYQVYLLHNNISVVGSSDFCPGHNTRYKASYSGLPS 301
DB 267 RELHLDNNKLTTRVPGLAHAKYQVYLLHNNISVVGQHDPCIPQTKSTYAVSLYS 326
QY 302 NPQVMEIOPSTFRCYVRSATQLGNKY 329
DB 327 NPVRYQHHPHTRCVFGRSTIQLGNKY 354
RESULT 12
PGS1 XENLA STANDARD; PRT; 368 AA.
AC Q9IB75;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Biglycan precursor.
GN BGN.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;

FT REPEAT 314 343 LRR-T 7.
 FT REPEAT 344 369 LRR-T 8.
 FT CARBOHYD 42 42 O-LINKED (GLYCOSAMINOGLYCAN) (BY
 FT CARBOHYD 48 48 SIMILARITY).
 FT CARBOHYD 271 271 O-LINKED (GLYCOSAMINOGLYCAN) (BY
 FT CARBOHYD 312 312 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 64 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 322 355 BY SIMILARITY.
 SQ SEQUENCE 369 AA; 41706 MM; 319DC15117PC604 CRC64;
 Query Match 57.5%; Score 985.5; DB 1; Length 369;
 Best Local Similarity 57.6%; Pred. No. 1.2e-62;
 Matches 190; Conservative 51; Mismatches 86; Indels 3; Gaps 2;
 QY 2 EASGIGPE--VPDRDPEPSLGPVCPFCQCHLHVOCSDLGKLVKVPDPTLLDQ 59
 DB 40 EASGSDTTSQVPLDLSLTPFSAMCPFGCHLHVOCSDLGKLVKVPDPTLLDQ 99
 QY 60 NNKTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLELYLSKNQKELPEKMP 119
 DB 100 NNDISELRKDFKGLQHLVYLVNNKISKHEKAFPLRLQKLYISKHVLVEIPNLP 159
 QY 120 KTLOELFAHENEITKAKVTPNGUNQMTVIELGNPLKSGCIENGAFQMGKLSYRIAD 179
 DB 160 SSVLELHIDNRIRKVPKGVSGIRNNMCIEGPNLENGFEPGARDGL-KLNYLRIS 218
 QY 180 TNITISFQGLPPLSTELHLDGNKISRVDASLKGANLAKGLSFNSISAVDNGSLANTP 239
 DB 219 AKLTGIRKDLPELTNELHIDNKKQALELDLRYSLKYLIGLGHNOIRMTENSLSFLP 278
 QY 240 HLRHLHLDNNKLTVPGLAEHKYIQVYLLNNNISVVGSDPFCPGHNTKKAASYGSVL 299
 DB 279 TLREHLHLDNNKLSHVPAGLPDLKILQVYLLHNNITKVGINDPFCMGFGVRAVYNGISL 336
 QY 300 PSNPVQWEIOPSTFRCCVYVSAIQLGNK 329
 DB 339 FNNVPVWEVQPAFRCVTRDLALQFQNYK 368
 RESULT 14
 PGSI_MOUSE STANDARD; PRT; 369 AA.
 AC P2865; Q61355;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Biglycan precursor (Bone/cartilage proteoglycan I) (PG-SI).
 GN BGN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NIH Swiss; TISSUE=Fibroblast;
 RA Naitoh Y., Suzuki S.;
 RL Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NIH Swiss; TISSUE=Embryo;
 RX MEDLINE=94319093; PubMed=8043960;
 RA Rau W., Just W., Vetter U., Vogel W.;
 RT "A dinucleotide repeat in the mouse biglycan gene (BST) on the X
 chromosome";
 RL Mamm. Genome 5:395-396(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast, and Kidney;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klauener R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavani P.L., Scheetz T.B.,
 RA Brownstein M.J., Udell T.B., Toehlyuk S., Carninci P., Prange C.J.,
 RA Raha S.S., Loguillano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wozniak K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywnicki M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 11-152 FROM N.A.
 RP STRAIN=C57BL/6;
 RX MEDLINE=21210929; PubMed=11311118;
 RA Saenaeen A.-M.K., Salminen H.J., Kantakokko A.J., Heinegaard D.,
 RA Vuorio E.I.;
 RT "Murine fibromodulin: cDNA and genomic structure, and age-related
 expression and distribution in the knee joint.";
 RL Biochem. J. 355:577-585(2001).
 CC -1- FUNCTION: May be involved in collagen fiber assembly (By
 similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
 similarity).
 CC -1- TISSUE SPECIFICITY: Found in several connective tissues, specially
 in articular cartilages.
 CC -1- PFM: The two attached glycosaminoglycan chains can be either
 chondroitin sulfate or dermatan sulfate (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
 (SLRP) FAMILY. CLASS I SUBFAMILY.
 CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
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 DR EMBL; X53928; CAA37875.1; -;
 DR EMBL; L20276; AAA64360.1; -;
 DR EMBL; BC005452; AAH05452.1; -;
 DR EMBL; BC019502; AAH19502.1; -;
 DR EMBL; Y11758; CAA72422.1; -;
 DR F1R; S20811; S20811.
 DR MGD; MGI:88158; Bgn.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000372; LRR Nterm.
 DR InterPro; IPR003591; LRR_cyp.
 DR Pfam; PF00560; LRR; 9
 DR Pfam; PF01462; LRRNT; 1.
 DR SMART; SM0013; LRRNT; 1.
 KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 KW Leucine-rich repeat; Signal.
 FT SIGNAL 1 19
 FT PROPEP 1 37
 FT CHAIN 38 369
 FT DOMAIN 64 77 BIGLYCAN.
 FT REPEAT 83 103 CYS-RICH.
 FT REPEAT 104 127 LRR-S 1.
 FT REPEAT 128 151 LRR-T 1.
 FT REPEAT 152 172 LRR-S 2.
 FT REPEAT 173 196 LRR-T 3.
 FT REPEAT 197 221 LRR-T 4.
 FT REPEAT 222 242 LRR-S 3.

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FT REPEAT 243 266 LRR-T 5.
FT REPEAT 267 290 LRR-T 6.
FT REPEAT 291 313 LRR-S 4.
FT REPEAT 314 343 LRR-T 7.
FT REPEAT 344 369 LRR-T 8.
FT CARBOHYD 42 42 O-LINKED (GLYCOSAMINOGLYCAN) (BY
SIMILARITY).
FT CARBOHYD 48 48 O-LINKED (GLYCOSAMINOGLYCAN) (BY
SIMILARITY).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 312 312 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 64 77 BY SIMILARITY.
FT DISULFID 322 355 BY SIMILARITY.
FT CONFLICT 68 68 C -> W (IN REF. 2).
SQ SEQUENCE 369 AA; 41639 MW; 4B57FCC9A102B86 CRC64;

Query Match 57.5%; Score 984.5; DB 1; Length 369;
Best Local Similarity 57.6%; Pred. No. 1.5e-62;
Matches 190; Conservative 51; Mismatches 86; Indels 3; Gaps 2;

OY 2 EASGIGPE--VPDDRPFPSLGPVCPFRQCHLRVVGCSGLGLDKVPKDLPPDTLLDQ 59
DB 40 EASGSDTTSGLPDDSLTPFTSAMCPFGCHGLRVVQCSGLGLKTPKELSPDTLLDQ 99
OY 60 NKKITEIKDGFKNLKNLHALILVNNKISKVSPGAFPLVLERLYLSKNQKELPEKMP 119
DB 100 NNDISELAKDDPKGLQHLYALVLYNNKISKIHEKAFSLRKLQKLYISKNLVLEIPNLP 159
OY 120 KTLQELRAHENEITVRKRVTEGNLQNVIELGTNPILKSGIENGAFQMKKLSYRIAD 179
DB 160 SSLVELRKHDRIRKRVKGVSGFLNMMNCIENGPNLENGPEGAFDGL-KLNTLRISE 218
OY 180 TNITSIPGGLPSSLTELHLNDNKISRVDASLKGINLAKGLSNISIAVNGSLANTP 239
DB 219 AKLTGIPDLPETLNEHLNDNKIQALBELDLRSKYRGLGNQRMENGLSFLP 278
OY 240 HLRRLHLDNNKLTFRVPGGLAEHKYIQVYVYLNHNNSIVGSSDFCPGNTKASYSYSL 299
DB 279 TLRELHLNNKLSRPAIGLIDKLQVYVYLSHNNITTKYGINDFCMGSGVRAYYNGISL 338
OY 300 FSNPQVWEIOPSTRCYVVSALQGNVYK 329
DB 339 FNNPVPWEVQFATERCVTLRLAIOFQVNYK 368

RESULT 15
PESI_HORSE STANDARD; PRT; 372 AA.
AC 046403; OSN1U5;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Biglycan precursor (Bone/cartilage proteoglycan I) (Pg-S1).
GN BGN.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_Taxid:9796;
RN [1]
RN SEQUENCE FROM N.A.
RA Richardson D.W., Dodge G.R.;
RT "Dose dependent effects of corticosteroids on the expression of matrix
RT related genes in equine articular chondrocytes.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE OF 150-192 FROM N.A.
RP MEDLINE=20082971; PubMed=10613847;
RA Caetano A.R., Shue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA Bowling A.T., Murray J.D.;
RT "A comparative gene map of the horse (Equus caballus).";
RL Genome Res. 9:1239-1249(1999).
CC -1- FUNCTION: May be involved in collagen fiber assembly (By
similarity).

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CC -1- SUBUNIT: Forms a ternary complex with MFAP2 and E1N (By
similarity).
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
similarity).
CC -1- PTM: The two attached glycosaminoglycan chains can be either
chondroitin sulfate or dermatan sulfate (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SMALL LUCICINE-RICH PROTEOGLYCAN
(SLRP) FAMILY. CLASS 1 SUBFAMILY.
CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
CC -----
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CC -----
CC EMBL; AF035934; AAB88305.1; -
CC EMBL; AF135020; AAF64248.1; -
CC InterPro; IPR001611; LRR.
CC InterPro; IPR000372; LRR_Nterm.
CC InterPro; IPR003591; LRR_Typ.
CC Pfam; PF00560; LRR; 8.
CC Pfam; PF01462; LRRNT; 1.
CC SMART; SMO0013; LRRNT; 1.
CC Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
CC Leucine-rich repeat; Signal.
CC SIGNAL 1 22
CC PROPEP 23 40
CC CHAIN 41 372
CC DOMAIN 67 80
CC REPEAT 86 106
CC REPEAT 107 130
CC REPEAT 131 154
CC REPEAT 155 175
CC REPEAT 176 199
CC REPEAT 200 224
CC REPEAT 225 245
CC REPEAT 246 269
CC REPEAT 270 293
CC REPEAT 294 316
CC REPEAT 317 346
CC REPEAT 347 372
CC CARBOHYD 45 45
CC FT FT O-LINKED (GLYCOSAMINOGLYCAN) (BY
FT FT SIMILARITY).
FT FT CARBOHYD 51 51
FT FT O-LINKED (GLYCOSAMINOGLYCAN) (BY
FT FT SIMILARITY).
DB 43 EASGADTTSGLPDDSLTPFTSAMCPFGCHGLRVVQCSGLGLKAVPEKISPDITLLDQ 102
OY 60 NKKITEIKDGFKNLKNLHALILVNNKISKVSPGAFPLVLERLYLSKNQKELPEKMP 119
DB 103 NNDISELAKDDPKGLQHLYALVLYNNKISKIHEKAFSLRKLQKLYISKNLVLEIPNLP 162
OY 120 KTLQELRAHENEITVRKRVTEGNLQNVIELGTNPILKSGIENGAFQMKKLSYRIAD 179
DB 160 SSLVELRKHDRIRKRVKGVSGFLNMMNCIENGPNLENGPEGAFDGL-KLNTLRISE 221
OY 180 TNITSIPGGLPSSLTELHLNDNKISRVDASLKGINLAKGLSNISIAVNGSLANTP 239
DB 219 AKLTGIPDLPETLNEHLNDNKIQALBELDLRSKYRGLGNQRMENGLSFLP 281

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QY 240 HURELHLDNNKLTTRVPGGLAEHKYIQVYTLHNNNISVGVSSDFCPGPHNTKASYSGVSL 299
 DB 282 TLREHLHLDNNKLSRPVAGIPDLKLLQVYVLTNNITKVGWDFCPVGVKRAYNGISL 341
 QY 300 FSNPVQWEIOPSTRFCYVVRSAIOLGNK 329
 DB 342 FNNPVYWEVOPATRCCTDRALIOGNK 371

RESULT 16
 PGSL SHEEP
 ID PGSL SHEEP STANDARD; PRT; 369 AA.
 AC 046390;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Biglycan precursor (bone/cartilage proteoglycan I) (PG-S1).
 GN BGN.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Choroid plexus;
 RA Bruet L., Clements J.E.;
 DT Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: May be involved in collagen fiber assembly. (By
 similarity).
 CC -1- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (by
 similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (by
 similarity).
 CC -1- TISSUE SPECIFICITY: Found in several connective tissues, specially
 in articular cartilages.
 CC -1- PTM: The two attached glycosaminoglycan chains can be either
 chondroitin sulfate or dermatan sulfate (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
 (SLRP) FAMILY. CLASS I SUBFAMILY.
 CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: AF034842; AAB87988.1; -.
 DR InterPro: IPR001611; LRR
 DR InterPro: IPR000372; LRR_Nterm.
 DR InterPro: IPR003591; LRR_Typ.
 DR Pfam: PF00560; LRR_8.
 DR Pfam: PF01462; LRRNT; 1.
 DR SMART: SM00013; LRRNT; 1.
 KM Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 KV Leucine-rich repeat; Signal.
 FT SIGNAL 1 19
 FT PROPEP 20 37
 FT CHAIN 38 369
 FT DOMAIN 64 77
 FT REPEAT 83 103
 FT REPEAT 104 127
 FT REPEAT 128 151
 FT REPEAT 152 172
 FT REPEAT 173 196
 FT REPEAT 197 221
 FT REPEAT 222 242
 FT REPEAT 243 266
 FT REPEAT 267 290
 RN LRR-T 6.

FT REPEAT 291 313 LRR-S 4.
 FT REPEAT 314 343 LRR-T 7.
 FT REPEAT 344 369 LRR-T 8.
 FT CARBOHYD 42 42 O-LINKED (GLYCOSAMINOGLYCAN) (BY
 FT CARBOHYD 48 48 SIMILARITY).
 FT CARBOHYD 48 48 O-LINKED (GLYCOSAMINOGLYCAN) (BY
 FT CARBOHYD 271 271 SIMILARITY).
 FT CARBOHYD 312 312 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 64 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 322 355 BY SIMILARITY.
 SQ SEQUENCE 369 AA; 41523 MW; 048C82C33909EB6 CRC64;
 Query Match 57.4%; Score 982.5; DB 1; Length 369;
 Best Local Similarity 57.3%; Pred. No. 2e-62;
 Matches 189; Conservative 51; Mismatches 87; Indels 3; Gaps 2;

QY 2 EASGIGPE--VDDRDFFPSLGPVCPFRQCHLRVYQSSDGLDRVPKDLPPDTLLDLQ 59
 DB 40 BASGAETTSGLPDLSDLPPTYSAMCPFGCHLRVYQSSDGLKAVPKAISPDITLLDLQ 99
 QY 60 NNTKEIWDGDPKLNKLNHALILVNNKISKSPGAFPLVKLERLYLSKNQKELPEKRP 119
 DB 100 NNDISELRKDPKGLQHLVAVLVNNKISKIHEKAFSPLRKQKLYISKHNLVRIIPNLP 159
 QY 120 KTLQELRAHENEITKRVKTFNGLNQMTVIELGTNPPLKSSGISENGAFQGMKLSYRIAD 179
 DB 160 SSVLRIRHNRIRKVPKGVBSGLNMMNCIENGSPLENSGEPGAFDEL-KLNTLRISL 218
 QY 180 TNITSIPQGLPSPTEHLHDGKNSRVDAAISLKLNTAKLGLSPNSISAVDNGSLANTP 239
 DB 219 AKLTGPKDLPELTNELHLDHNKIQALELDLRLRSKLYRGLGHNGQRMINGSLSPFP 278
 QY 240 HURELHLDNNKLTTRVPGGLAEHKYIQVYTLHNNNISVGVSSDFCPGPHNTKASYSGVSL 299
 DB 279 TLREHLHLDNNKLSRPVAGIPDLKLLQVYVLTNNITKVGWDFCPVGVKRAYNGISL 338
 QY 300 FSNPVQWEIOPSTRFCYVVRSAIOLGNK 329
 DB 339 FNNPVYWEVOPATRCCTDRALIOGNK 368

RESULT 17
 PGSL HUMAN
 ID PGSL HUMAN STANDARD; PRT; 368 AA.
 AC P21810; P13247;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Biglycan precursor (bone/cartilage proteoglycan I) (PG-S1).
 GN BGN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone;
 RX MEDLINE=89174714; PubMed=2647739;
 RA Fisher L.W., Terhune J.D., Young M.F.;
 RT "Deduced protein sequence of bone small proteoglycan I (biglycan)
 RT shows homology with proteoglycan II (decorin) and several
 RT nonconnective tissue proteins in a variety of species.";
 RL J. Biol. Chem. 264:4571-4576 (1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91317791; PubMed=1860845;
 RA Fisher L.W., Heggard A.M., Vetter U., Vogel W., Just W.,
 RA Terhune J.D., Young M.F.;
 RT "Human biglycan gene. Putative promoter, intron-exon junctions, and
 RT chromosomal localization.";
 RL J. Biol. Chem. 266:14371-14377 (1991).
 RN [3]

RP SEQUENCE FROM N.A.
 RX MEDLINE=20314869; PubMed=10854409;
 RA Mollon A.M., Platzer M., Bates R., Gloeckner G., Botcherby M.,
 RA Nordstiek G., Strivens M.A., Kioschis P., Dangel A., Cunningham D.,
 RA Straw R., Weston P., Hunter C., Gilbert M., Fernando S., Goodall K.,
 RA Kerry G., Greystrong J.S., Clark D., Goerds M., Blechschmidt K.,
 RA Rump A., Hinman B., Mundy C.R., Miller W., Fouscka A., Herman G.E.,
 RA Rhodes M., Denny P., Rosenthal A., Brown S.D.M.,
 RT "Comparative genome sequence analysis of the Bpa/Str region in mouse
 RT and man.";
 RL Genome Res. 10:758-775(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strauberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Sepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Caminci P., Prange C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Rahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Biochem. J. 262:823-827(1989).
 RN [6]
 RP SEQUENCE OF 38-57.
 RX MEDLINE=90073579; PubMed=2590169;
 RA Roughley P.J., White R.J.,
 RT "Dermapan sulphate proteoglycans of human articular cartilage. The
 RT properties of dermapan sulphate proteoglycans I and II.";
 RL Biochem. J. 262:823-827(1989).
 RN [7]
 RP SEQUENCE OF 38-66.
 RX MEDLINE=87250639; PubMed=3597437;
 RA Fisher L.W., Hawkins G.R., Turcos N., Termine J.D.,
 RT "Purification and partial characterization of small proteoglycans I
 RT and II, bone sialoproteins I and II, and osteonectin from the mineral
 RT compartment of developing human bone.";
 RL J. Biol. Chem. 262:9702-9708(1987).
 RN [7]
 RP SEQUENCE OF 361-368 FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=95187185; PubMed=7881444;
 RA Just W., Rau W., Muller R., Geerkens C., Vogel W.,
 RT "Idiotype repeat polymorphism at the human biglycan (BGN)
 RT locus.";
 RL Hum. Mol. Genet. 3:2268-2268(1994).
 CC -1- FUNCTION: May be involved in collagen fiber assembly (By
 CC similarity).
 CC -1- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
 CC similarity).
 CC -1- TISSUE SPECIFICITY: Found in several connective tissues, specially
 CC in articular cartilages.
 CC -1- PTM: The two attached glycosaminoglycan chains can be either
 CC chondroitin sulfate or dermatan sulfate (By similarity).
 CC (SLRP) FAMILY. BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
 CC (SLRP) FAMILY. CLASS 1 SUBFAMILY.
 CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
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 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@1sb-sib.ch).
 CC -----
 DR EMBL: J04599; AAA3609.1; -;
 DR EMBL: M65153; AAA5287.1; ALT SEQ.
 DR EMBL: M65152; AAA5287.1; JOINED.
 DR EMBL: U82695; -; NOT ANNOTATED CDS.
 DR EMBL: BC002416; AA02416.1; -;
 DR EMBL: BC004244; AA04244.1; -;
 DR EMBL: U11686; AAC50117.1; -;
 DR PIR: A40757; BGNUN.
 DR Genew; HGNC:1044; BGN.
 DR MIM: 301870; -;
 DR GO: GO:0005578; C:extracellular matrix; NAS.
 DR GO: GO:0005201; F:extracellular matrix structural constituent; NAS.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR00372; LRR_Nterm.
 DR InterPro: IPR003591; LRR_Typ.
 DR Pfam: PF00560; LRR; 9.
 DR Pfam: PF01462; LRRNT; 1.
 DR SMART: SM00013; LRRNT; 1.
 KW Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 KW Leucine-rich repeat; Signal.
 FT SIGNAL 1 19
 FT PROPEP 20 37
 FT CHAIN 38 368
 FT DOMAIN 63 76
 FT REPEAT 82 102
 FT REPEAT 103 126
 FT REPEAT 127 150
 FT REPEAT 151 171
 FT REPEAT 172 195
 FT REPEAT 196 220
 FT REPEAT 221 241
 FT REPEAT 242 265
 FT REPEAT 266 289
 FT REPEAT 290 312
 FT REPEAT 313 342
 FT REPEAT 343 368
 FT CARBOHYD 42 42
 FT CARBOHYD 47 47
 FT CARBOHYD 270 270
 FT CARBOHYD 311 311
 FT DISULFID 63 76
 FT DISULFID 321 354
 FT CONFLICT 139 140
 FT CONFLICT 163 164
 FT SEQUENCE 368 AA; 41654 MW; BFL6F304C5CD3B3E CRC64;
 SO
 Query Match 57.2%; Score 979; DB 1; Length 368;
 Best Local Similarity 57.4%; Pred. No. 3.6e-62;
 Matches 189; Conservative 50; Mismatches 88; Indels 2; Gaps 2;
 Db 2 EASGIGPE-VDDRDFEPPSLGAPVCPFRQCHLRVQCSIDGLDVPKPLDPTLLDQ 60
 40 EASGADSVGLDPPSVPTPTASAMCPFGCHLRVQCSIDGLKSVKPSIDPTLLDQ 99
 61 NKTTEIDGPKLNKLNIAHLLVNNKSKVSPGAFVLYGLERYLKNQKELPECKPK 120
 100 NDISELKKDPEFGQIHLYAVLVNNKISKIHERKPSLRKQKLYIKRNLVETLPP 159
 121 TLQELRAHENVITKRVATFNGLNQMVIELGTNPLSSGIENGAPQGMKKLSTYRIADT 180
 160 SLVFLRLHDKRIRKRVPGVSGLANMCIEMGNGPLNSGFEPAFGL-KLNTLRISBA 218
 181 NITSIPQGLPPLSLTELHDKNKSIRVDASLKGIANLAKLGLSNSSISAVNGSLANTPH 240
 219 KLTGIPDLPETLHDLHDKIKQATLEDLRLRSKLYRIGLGNQRMTEINGSLSTPLPT 278

RA Henry S.P., Takanosu M., Boyd T.C., Mayne P.M., Eberspacher H.,
 RA Zhou W., de Crombrughe B., Hoeoek M., Mayne R.;
 RT "Expression pattern and gene characterization of asporin. A newly
 RT discovered member of the leucine-rich repeat protein family.",
 RL J. Biol. Chem. 276:12212-12221(2001).
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -1- TISSUE SPECIFICITY: Higher levels in osteoarthritic articular
 CC cartilage, aorta, uterus. Moderate expression in small intestine,
 CC heart, liver, bladder, ovary, stomach, and in the adrenal,
 CC thymoid, and mammary glands. Low expression in trachea, bone
 CC marrow, and lung.
 CC -1- PTM: Does not contain a serine/glycine dipeptide sequence required
 CC for the assembly of O-linked glycosaminoglycans and is probably
 CC not a proteoglycan. The N-linked glycan at Asp-281 is composed of
 CC variable structures of GlcNAc, mannose, fucose, HexNAc and hexose.
 CC -1- POLYMORPHISM: The poly-Asp region of ASPN is polymorphic and
 CC ranges at least from 11 to 17 Asp.
 CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
 CC (SLRP) FAMILY. CLASS I SUBFAMILY.
 CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
 CC -----
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 CC -----
 DR EMBL: AF316824; AAK5161.1; -;
 DR EMBL: AY029191; AAK31800.1; -;
 DR EMBL: AK027359; BAB5060.1; -;
 DR Genew: HGNC:14872; ASPN.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR003372; LRR_Nterm.
 DR InterPro: IPR003591; LRR_Cyp.
 DR Pfam: PF00560; LRR_8.
 DR Pfam: PF01462; LRRNT_1.
 DR SMART: SM00013; LRRNT_1.
 DR GlycoProtein: Extracellular matrix; Signal; Repeat;
 KW leucine-rich repeat; Polymorphism; Triplet repeat expansion.
 FT SIGNAL 1 14
 FT PROPEP 15 32
 FT CHAIN 33 379
 FT DOMAIN 76 89
 FT REPEAT 95 115
 FT REPEAT 116 139
 FT REPEAT 140 163
 FT REPEAT 164 185
 FT REPEAT 185 208
 FT REPEAT 209 233
 FT REPEAT 234 254
 FT REPEAT 255 278
 FT REPEAT 279 302
 FT REPEAT 303 325
 FT REPEAT 326 355
 FT REPEAT 356 379
 FT DISULFID 332 365
 FT DOMAIN 36 52
 FT CARBOHYD 54 54
 FT CARBOHYD 281 281
 FT CONFLICT 237 242
 FT SEQUENCE 379 AA; 43302 MW; 786625859E26A56D CRC64;
 SQ
 Query Match 55.1%; Score 943.5; DB 1; Length 379;
 Best Local Similarity 55.0%; Pred. No. 1.2e-59;
 Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;
 QY 11 PDDRDEPSLGPVPCRCOCHLRVYVCSLDGLDXYVKDLPPTTLIDLNNTTETKQD 70
 DB 61 PSHHPFPLFPKCPGCGCCYKRVHCSLDGLSVTTLIPPTRMIDLNNTTETKEND 120
 QY 71 FKNLKNLHLLVNNKISKVSPPAFTPLVETLRYLTKNQLKELPEKMKETIQELRAHNN 130

DB 121 FGLGISVGLIANNKTKRKHKAPLUTTKLARLILSHNQSLSEIPLNPKSLAEIRIHNN 180
 QY 131 EITTKRYKTNGLNOMIVIELGTNPVKSSGIENGAPQGMKLSYRIADNTITSIPQGP 190
 DB 181 KYKKIIOKTFKGMNLAHLVEMSANPLDNNNGIEPGAEGV-TVFHIRIAEAKLTVKGP 239
 QY 191 PELTEHLIDGNKISVDAASLKLNNLAKLGSPFISAVNDGSLANTPHLEHLDNNK 250
 DB 240 FTLEHLADYNTKISTVELDEDFRYEQLRGLGNKKITDIEGSLANIPRAVEHLNNK 299
 QY 251 LTRVPGLAENHYIOVVYLNHNNISVGSDDPCPGHNTKKASVGSVLSFNPVQWEIO 310
 DB 300 LKKISGLPELKYGLIIFLHSSISARVGVNDPCFVPRKKSYSALISFNPNVYKWEQ 359
 QY 311 PETPRCYVRSAIQLGNTY 328
 DB 360 PATPRCVLSRMSVQLGNF 377
 RESULT 21
 ASPN_MOUSE STANDARD; PRT; 373 AA.
 AC 099M04; Q9D6A2;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Asporin precursor.
 GN ASPN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciognathi; Muridae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X 129/SvJ; TISSUE=Aorta;
 RX MEDLINE=21192276; PubMed=11152692;
 RA Lorenzo P., Asperberg A., Oemerford P., Bayliss M.T., Neame P.J.,
 RA Heinegaard D.;
 RT Identification and characterization of asporin. A novel member of the
 RT leucine-rich repeat protein family closely related to decorin and
 RT biglycan.";
 RL J. Biol. Chem. 276:12201-12211(2001).
 RN [2]
 RP SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.
 RC MEDLINE=21192277; PubMed=11152695;
 RX Henry S.P., Takanosu M., Boyd T.C., Mayne P.M., Eberspacher H.,
 RA Zhou W., de Crombrughe B., Hoeoek M., Mayne R.;
 RT "Expression pattern and gene characterization of asporin. A newly
 RT discovered member of the leucine-rich repeat protein family.";
 RL J. Biol. Chem. 276:12212-12221(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shitagawa A., Shibata K., Yoshino M., Toch M., Ishii Y.,
 RA Arakawa T., Hara A., Fukumishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Steubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guslinich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Momberts P.,
 RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
 RA Hayashizaki Y.;

CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=9909324; PubMed=9790758;
 RA Nishikawa J., Tanaka T., Nakamura Y.;
 RT "Identification of a novel gene (ECM2) encoding a putative
 RT extracellular matrix protein expressed predominantly in adipose and
 RT female-specific tissues and its chromosomal localization to 9q22.3.";
 RL Genomics 52:378-381 (1998).
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -1- TISSUE SPECIFICITY: Expressed predominantly in adipose tissue as
 CC well as female-specific organs such as mammary gland, ovary, and
 CC uterus.
 CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCANS
 CC (SLRPs) FAMILY.
 CC -1- SIMILARITY: Contains 1 VWF domain.
 CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
 CC -----
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 CC -----
 CC EMBL; AB011792; BAA33958.1; -
 CC GenBank; HGNC:3154; ECM2.
 DR MIM; 603479; -
 DR GO; GO:0005578; C:extracellular matrix; TAS.
 DR GO; GO:0005178; F:integrin binding activity; TAS.
 DR GO; GO:0007160; P:cell-matrix adhesion; TAS.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR003591; LRR_Cyp.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF00560; LRR; 10.
 DR Pfam; PF00093; VWF; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00214; VWC; 1.
 DR PROSITE; PS01208; VWF_1; 1.
 DR PROSITE; PS50184; VWF_2; 1.
 DR Leucine-rich repeat; Repeat; Glycoprotein; Extracellular matrix;
 KM Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 1 699 EXTRACELLULAR MATRIX PROTEIN 2.
 FT DOMAIN 101 158 VWC.
 FT REPEAT 335 355 LRR-S 1.
 FT REPEAT 356 379 LRR-T 1.
 FT REPEAT 382 405 LRR-T 2.
 FT REPEAT 406 426 LRR-S 2.
 FT REPEAT 427 450 LRR-T 3.
 FT REPEAT 451 476 LRR-T 4.
 FT REPEAT 477 497 LRR-S 3.
 FT REPEAT 524 547 LRR-T 5.
 FT REPEAT 556 596 LRR-T 6.
 FT REPEAT 621 643 LRR-S 4.
 FT REPEAT 644 672 LRR-T 7.
 FT REPEAT 673 699 LRR-T 8.
 FT SITE 270 281 POLY-GUT.
 FT SITE 294 296 CELL ATTACHMENT SITE (POTENTIAL).
 FT CARBOHYD 378 378 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 449 449 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 506 506 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 699 AA; 79789 MW; E44E76A40A5C2742 CRC64;
 Query Match 22.7%; Score 389; DB 1; Length 699;
 Best Local Similarity 27.0%; Pred. No. 4.3e-20;
 Matches 113; Conservative 58; Mismatches 144; Indels 104; Gaps 9;

QY 47 KOLPPTLLDQNNKITEIKDQFQNTKNTALLVNNKI--SKVSPGAFPTLVKLERL 104
 DB 339 PLTAPQITSLTELGNSIASIPDEAFNGLNLRDLDSKNITSSGGIPAFKLLKLMKL 398
 QY 105 YLSKQKLELPKMPKTIQELRAHENEITKVKYTFNGNQMIIVIELGNPKSSGIENG 164
 DB 399 NNDGNLILQIPQGLPSTLELVNENNLQADIESISDNLQVLELBNNTSEANVNL 458
 QY 165 AFQMKGLSYITLADNTITSIPQGLPSTLELVNENNLQADIESISDNLQVLELBNNTSEANVNL 207
 DB 459 AFQMKGLSYITLADNTITSIPQGLPSTLELVNENNLQADIESISDNLQVLELBNNTSEANVNL 518
 QY 208 -----NLSKGLN--NLSKGLSPNS----- 227
 DB 519 NLSKGLN--NLSKGLSPNS----- 227
 QY 228 -----SAVNGSLANTPH--LREIHLNNKLTVPVGGIAEHKVIQVYL 269
 DB 579 MERGLELYLSTNNKLAADGMDVSPFGAHSRLRLFDNDLKSIPPGIOEMKALHFLKL 638
 QY 270 HNNNTSVGSSDFCPPEGHNTKASYSVGS--LFSNPQVWEIQPSTFCVYVRSATQL 325
 DB 639 NNNKLTNNIPERIC-----NAEEDDSNLEHLLENNYIKIRIPSTVFCIRSYSIVL 693
 RESULT 26
 ID PRP MOUSE STANDARD; PRT; 378 AA.
 AC Q9JK53;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Prolargin precursor (proline-arginine-rich end leucine-rich repeat
 DE protein).
 GN PRP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP MEDLINE=21588626; PubMed=11731272;
 RX GROVER J., ROUGHLEY P.J.;
 RA "Characterization and expression of murine PRP.",
 RL Matrix Biol. 20:555-564 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary gland;
 RX MEDLINE=22388257; PubMed=12477932;
 RA STRAUSBERG R.L., FEINGOLD E.A., GROUSE L.H., DERGE J.G.,
 RA KLAUSNER R.D., COLLINS F.S., WAGNER L., SHERMAN C.M., SCHULER G.D.,
 RA ALTSCHUL S.F., ZEEBERG B., BUETOW K.H., SCHEFFER C.F., BHAT N.K.,
 RA HOPKINS R.F., JORDAN H., MOORE T., MAX S.I., WANG J., Hsieh F.,
 RA DIATCHENOV L., MARUSINA K., FARMER A.A., RUBIN G.M., HONG L.,
 RA STRAUSSBERG M., SOARES M.B., BONALDO M.F., CAEVARTE T.L., SCHEETZ T.B.,
 RA BROWNSTEIN M.J., USIDIN T.B., TOSHIYUKI S., CARMICHAEL P., PRANGE C.,
 RA RAHA S.S., MCLELLAN N.A., PETERS G.J., MALEK J.A., GUNARATNE P.H.,
 RA RICHARDS S., WOLLEY K.C., HALE S., GARCIA A.M., GAY L.J., HULYK S.W.,
 RA VILLALON D.K., MURPHY D.M., SODERGREN E.J., LU X., GIBBS R.A.,
 RA PAHEY J., HELTON E., KETTEMAN M., MADAN A., RODRIGUES S., SANCHEZ A.,
 RA WHITING M., MADAN A., YOUNG A.C., SHEVCHENKO Y., BOUFFARD G.G.,
 RA BLAKESLEY R.W., TOUCHMAN J.W., GREEN E.D., DICKSON M.C.,
 RA RODRIGUEZ A.C., GRIMWOOD J., SCHMUTZ J., MYERS R.M.,
 RA BUTTERFIELD V.S.G., KRZYWINSKI M.I., SKALSKA U., SMILLUS D.E.,
 RA SCHNERCH A., SCHEIN J.E., JONES S.J.M., MARTA M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: May anchor basement membranes to the underlying
 CC connective tissue (By similarity).
 CC -1- SUBUNIT: Binds the basement membrane heparan sulfate proteoglycan

CC perlecan and triple helical collagens type I and type II (By
CC similarity).

CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -1- TISSUE SPECIFICITY: Expressed in cartilage throughout both fetal
CC development and post-natal life. It is also expressed in the
CC developing embryo prior to skeletogenesis. In adult, highest
CC expression in lung, lower levels in cardiac and skeletal muscle.
CC -1- DOMAIN: The basic amino-terminal Arg/Pro-rich binds heparin and
CC heparan sulfate. Binds collagens type I and type II through its
CC leucine-rich repeat domain (By similarity).

CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC (SLRP) FAMILY, CLASS II SUBFAMILY.
CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.

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CC -----
CC EMBL: AF261887; AAF72994.2; JOINED.
CC EMBL: AF261887; AAF72994.2; JOINED.
CC EMBL: BC019775; AAH19775.1; --.
CC MGI: MGI:2151110; PRELP.
CC InterPro: IPR001611; LRR.
CC InterPro: IPR00372; LRR_Nterm.
CC InterPro: IPR003591; LRR_Typ.
CC Pfam: PF00560; LRR_7.
CC Pfam: PF01462; LRRNT_1.
CC SMART: SM00013; LRRNT_1.
CC GlycoProtein; Extracellular matrix; Repeat; leucine-rich repeat;
CC signal.

KM SIGNAL. 1 21 POTENTIAL.
FT CHAIN 22 378 PROLARGIN.
FT DOMAIN 69 85 LRR-S 1.
FT REPEAT 91 110 LRR-S 1.
FT REPEAT 111 134 LRR-T 1.
FT REPEAT 135 158 LRR-T 2.
FT REPEAT 159 179 LRR-S 2.
FT REPEAT 180 203 LRR-T 3.
FT REPEAT 204 229 LRR-T 4.
FT REPEAT 230 250 LRR-S 3.
FT REPEAT 251 274 LRR-T 5.
FT REPEAT 275 299 LRR-T 6.
FT REPEAT 300 319 LRR-S 4.
FT REPEAT 320 358 LRR-T 7.
FT REPEAT 359 378 LRR-T 8.
FT DOMAIN 193 198 POLY-LIU.
FT DISULFID 328 369 BY SIMILARITY.
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 316 316 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 323 323 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 378 AA; 43292 MW; 81654PB9DF55186 CRC64;

Query Match 22.6%; Score 386.5; DB 1; Length 378;
Best Local Similarity 32.2%; Pred. No. 2.9e-20;
Matches 93; Conservative 57; Mismatches 124; Indels 15; Gaps 6;

QY 2 BASGIGPEVDDRDDEPSIGPVCPFRCCQ---HLEVVQCSDLGLDKVPEKLPDPTLLDL 58
DB 50 EPTDLPPLPPG---PSSVFPDCPRECYCPDPFSAALYCDSSNLARVPV-IPPRHLYL 105
DB 59 QNNKTEKXGDGFKLKNLHLLVNNKISKVSPGAFPLVLEKLYLSKNOJKEPPEM 118
QY 106 QNNFTTEELPESFQWATGRLRWNLNLRKRDQVGLGLPSLAPLYMEKNOJLEVPSSL 165
DB 119 PPTLQELRAHEVEIKVRKVTENGNNOMVIELGNTPLKSGSIEGNGAFQMKGLSYTIA 178
QY 166 PNNLQRLSLQNLISRIIPGVSKLBNLLLDLQNNRLSDGVFKADTFQGLKNLMQNLDA 225

QY 179 DNTITSIQGLPSTLHLDONKISRVDASLGIANNLALGLSFNSISAVDNG---SL 235
DB 226 HNLIRKMPKVPQAIHQLYLDSNKIETIPNGYFDFPPLAFIRNNYNLGS--DRGLPKNS 283
QY 236 ANTPHRLREHLDNNKLTFRVPGGLAEHKYIQVYVLIHNNNISVVGSSDFCP 284
DB 284 FNISNLVLIHLSHKKISNVP---ALSNGLREHLYNNNISIEKINGTQICP 329

RESULT 27
PRELP_HUMAN STANDARD; PRT; 362 AA.
ID PRELP_HUMAN
AC PS1868;
DT 01-OCT-1996 (Rel. 34, Created)
DR 01-OCT-1996 (Rel. 34, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Prolagin precursor (Proline-arginine-rich end leucine-rich repeat
DE protein).
GN PRELP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96029653; PubMed=7592739;
RA Bengtsson E., Neame P.J., Heinegaard D., Sommerlin Y.;
RT "The primary structure of a basic leucine-rich repeat protein, PRELP,
RT found in connective tissues.";
RL J. Biol. Chem. 270:25639-25644(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97127584; PubMed=8954791;
RA Grover J., Chen X.-N., Korenberg J.R., Recklies A.D., Roughley P.J.;
RT "The gene organization, chromosome location, and expression of a
RT 55-kDa matrix protein (PRELP) of human articular cartilage.";
RL Genomics 38:109-117(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=PANCREAS, AND Spleen;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein W.J., Ueda T.B., Tomihyuki S., Carninci P., Frange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halys S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: May anchor basement membranes to the underlying
CC connective tissue (By similarity).
CC -1- SUBUNIT: Binds the basement membrane heparan sulfate proteoglycan
CC perlecan and triple helical collagens type I and type II (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -1- TISSUE SPECIFICITY: Connective tissue.
CC -1- DOMAIN: The basic amino-terminal Arg/Pro-rich binds heparin and
CC heparan sulfate. Binds collagens type I and type II through its
CC leucine-rich repeat domain (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
CC (SLRP) FAMILY, CLASS II SUBFAMILY.

CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
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DR EMBL; U25089; AAC50230.1; -
 DR EMBL; U41344; AAC18782.1; -
 DR EMBL; U41343; AAC18782.1; JOINED.
 DR EMBL; BC032498; AAC2498.1; -
 DR PIR; I39068; I39068.
 DR Genew; HGNC:9357; FREDP.
 DR MIM; 601914; -
 DR GO; GO:0005578; C:extracellular matrix; TAS.
 DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
 DR GO; GO:0001501; P:skeletal development; TAS.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000372; LRR_Nterm.
 DR Pfam; PF00560; LRR; 8.
 DR SMART; SM00013; LRRNT; 1.
 DR Glycoprotein; Extracellular matrix; Repeat; Leucine-rich repeat;
 KM Signal; Polymorphism.
 FT SIGNAL 1 20
 FT CHAIN 21 382
 FT DOMAIN 73 89
 FT REPEAT 95 114
 FT REPEAT 115 138
 FT REPEAT 139 162
 FT REPEAT 163 183
 FT REPEAT 184 207
 FT REPEAT 208 233
 FT REPEAT 234 254
 FT REPEAT 255 278
 FT REPEAT 279 303
 FT REPEAT 304 323
 FT REPEAT 324 362
 FT REPEAT 363 382
 FT DOMAIN 197 202
 FT DISULFID 332 373
 FT CARBOHYD 124 124
 FT CARBOHYD 289 289
 FT CARBOHYD 320 320
 FT CARBOHYD 327 327
 FT VARIANT 348 348
 FT
 SQ SEQUENCE 382 AA; 43809 MW; A1C4E16B7515695 CRC64;
 Query Match 22.5%; Score 385.5; DB 1; Length 382;
 Best Local Similarity 31.5%; Pred. No. 3,4e-20;
 Matches 91; Conservative 59; Mismatches 124; Indels 15; Gaps 6;

QY 2 BAAGIGPEVDDDDPESLGPVCPFCQC--HRRVQSGDLGDKVPKLPDPTLLDL 58
 DB 54 EPTDLPPLPPG--PPSIRPPDCPRECPCPPDPSPALYCDSRMIRKPVV-IPRIHYLY 109
 QY 59 QNNKITEIKGDFPKNLKHALILVNNKISKVSPGAFPIVYKLERLYLSNOLKEPEKM 118
 DB 110 QNNPITLPPVESQNTGLKWINLNNRIRKIDQRYLEKIPGLVFLYMERNOLEVPASAL 169
 QY 119 PKTLQELRAHENEITKRVKTYFNQMIIVIEIGTNPILKSSGIENGAFQMKLSYIRLA 178
 DB 170 PRNLEQRLSQNHISRIPEGVFSKENTLLLDLQHNRISGVGKRPDTFGLKNTQNLNLA 229
 QY 179 DNYITSLPQGLPSLTLEHLDGKNSRVDAASLGLNNLAKLGLSFNSISAVDNG--SL 235
 DB 230 HNLIRKMPPEVPAHQLYLDSNKRITIPNGVFKSPKPSNLAIFRLNNTKLT--DRGLPKNS 287
 QY 236 ANTPHRLHLDNNKLTTRVPGGLAEHKYIQVVYLNHNNTSVGSSDPCP 284

DB 288 FNISNLVHLHSNRISVP--AINNRLEHLNHNNTSEKINGTOICP 333
 RESULT 28
 PGSI_RABIT
 ID PGSI_RABIT STANDARD; PRT; 135 AA.
 AC 046377;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Bg1lycan (Bone/cartilage proteoglycan I) (Pg-S1) (Fragment).
 GN BGN.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_Taxid=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand white;
 RX MEDLINE=99037997; PubMed=9822203;
 RA Boykitt R.H., Sciore P., Reno C.R., Marchuk L., Frank C., Hart D.A.;
 RT "Altered levels of extracellular matrix molecules MENA in healing
 RL rabbit ligaments."
 RL Matrix Biol. 171:371-378(1998).
 CC -1- FUNCTION: May be involved in collagen fiber assembly (By
 CC similarity).
 CC -1- SUBUNIT: Forms a ternary complex with MFAP2 and ELN (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
 CC similarity).
 CC -1- TISSUE SPECIFICITY: Found in several connective tissues, specially
 CC in articular cartilages.
 CC -1- PTM: The two attached glycosaminoglycan chains can be either
 CC chondroitin sulfate or dermatan sulfate (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
 CC (SLRP) FAMILY. CLASS I SUBFAMILY.
 CC -1- SIMILARITY: Contains at least 6 leucine-rich (LRR) repeats.
 CC
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 CC use by non-profit institutions as long as its content is in no way
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DR EMBL; AF020290; AAC39515.1; -
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR003591; LRR_LYP.
 DR Pfam; PF00560; LRR; 4.
 KM Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 FT LEUCINE-RICH REPEAT.
 FT NON_TER 1 1
 FT REPEAT 1 15
 FT REPEAT 16 15
 FT REPEAT 37 60
 FT REPEAT 61 84
 FT REPEAT 85 107
 FT REPEAT 108 135
 FT NON_TER 135 135
 SQ SEQUENCE 135 AA; EFDC6E74D42F5098 CRC64;
 Query Match 22.2%; Score 381; DB 1; Length 135;
 Best Local Similarity 54.5%; Pred. No. 1.8e-20;
 Matches 72; Conservative 24; Mismatches 36; Indels 0; Gaps 0;

QY 171 KLSYRIADNTITSIPQGLPSLTLEHLDGKNSRVDAASLGLNNLAKLGLSFNSISAV 230
 DB 4 KSNYLRISBAKLTGIPKDPETLANELHLDHNKIQAIELEDLRYSKLYLGLGHQIRMI 63
 QY 231 DNGSLANPHLAEHLDDNNKLTTRVPGGLAEHKYIQVVYLNHNNTSVGSSDPCP 290

DB 64 ENGLSELPTLREHLNNTKLSRVAGLPDLKLVYLLHSNNITKGVNDPCFVGK 123

QY 291 KASYSVGLFSN 302

DB 124 RAYNGISLFSN 135

RESULT 29

LUM_COTUA STANDARD; PRT; 343 AA.

AC Q9DE67;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Luminan precursor (Keratan sulfate proteoglycan Luminan). (KSPG Luminan).

GN LUM OR LDC.

OS Coturnix coturnix japonica (Japanese quail).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Coturnix.

OC NCBI_TaxID=93934;

OX [1]

RN SEQUENCE FROM N.A.

RP TISSUE=Cornea;

RX MEDLINE=20556471; PubMed=11102759;

RA Corpeuz L.M., Dunley J.R., Hassell J.R., Conrad A.H., Conrad G.W.;

RT "Molecular cloning and relative tissue expression of decorin and Luminan in embryonic quail cornea."

RL Matrix Biol. 19:699-704(2000).

CC -1 SUBUNIT: Binds to laminin (By similarity).

CC -1 SUBCELLULAR LOCATION: Secreted; extracellular matrix (By similarity).

CC -1 PTM: Binds keratan sulfate chains (By similarity).

CC -1 SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN (SLRP) FAMILY. CLASS 12 SUBFAMILY.

CC -1 SIMILARITY: Contains 12 leucine-rich (LRR) repeats.

CC -----

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CC -----

CC EMBL; AF125251; AAG48155.1; -

DR InterPro; IPR001611; LRR.

DR InterPro; IPR00372; LRR_Nterm.

DR InterPro; IPR003591; LRR_Typ.

DR Pfam; PF00560; LRR; 10.

DR Pfam; PF01462; LRRNT; 1.

DR SMART; PR00019; LEUCICRPT.

DR SMART; SMO0369; LRR_Typ; 1.

DR SMART; SMO0013; LRRNT; 1.

KM Glycoprotein; Extracellular matrix; Proteoglycan; Repeat; Leucine-rich repeat; Signal.

FT SIGNAL 1 18

FT CHAIN 19 343

FT DOMAIN 40 56

FT REPEAT 62 81

FT REPEAT 82 105

FT REPEAT 106 131

FT REPEAT 132 152

FT REPEAT 153 176

FT REPEAT 177 201

FT REPEAT 202 222

FT REPEAT 223 246

FT REPEAT 247 271

FT REPEAT 272 291

FT REPEAT 292 321

FT REPEAT 322 343

FT DISULFID 300 333

BY SIMILARITY.

FT CARBOHYD 91 91

FT FT

FT CARBOHYD 130 130

FT FT

FT CARBOHYD 165 165

FT FT

FT CARBOHYD 257 257

FT FT

FT CARBOHYD 320 320

FT SEQUENCE 343 AA; 38642 MW; A95199C7P32B7C4C CRC64;

Query Match 21.5%; Score 367.5; DB 1; Length 343;

Best Local Similarity 31.9%; Pred. No. 5.5e-19;

Matches 108; Conservative 58; Mismatches 146; Indels 27; Gaps 11;

QY 4 SGI-----GREVDDDDFEPSLGP---VCFPRQCHL---RVQCGSLGLDKYPKDLP 51

DB 14 SGIFQYDYP--ADDYGYDP-FGPSTAVCAPBCNCPSTPTAMYCDMLKUTIP-IVPS 69

QY 52 DTLTLDLNNKTKTEIKQDGFNLKALILVNNKI--SKVSPGAFPLVLERLYSKN 109

DB 70 GIKYLYRANMIBSIEBTFPNVTDLQMLIDHNLHNSKIKGVFSGLKMLKTLHINY 129

QY 110 QLKELPERMPKTLQELRAHENEITKRVKVTENGINQIVIELGTNPPLKSSGIENGAFQGM 169

DB 130 NLTEAVGFLPKTLDDLQLSHKIKTKVNPGLVNLVTLVHLLQNNQLKADSI-SGAFKGL 188

QY 170 KKLSTYIRADTNITISFQGLPPLSTELHDGSKISRDVDSLKGLNLAKLGLSPNLSA 229

DB 189 NSLYLYDSFNQTLPTGLPHSLIMLYFDNNQISNPDEYFQGFKTLQYLRLSHNTLT- 247

QY 230 VDN---GSLATPHLREHLNNTKLSRVAGLPDLKLVYLLHSNNITKGVNDPCFVGK 286

DB 248 -DSGIPGVNFTSLVELDLSFNQKSLP---TSENLENYLLQNNKINKPLSPFCVY 303

QY 287 HNTKASYSVGLFSNPNQYWEIQSPFCVYVSAIQI 325

DB 304 GPLYTSKTLRLDGNNTLRADLPQEWYNCIRVAABISL 342

RESULT 30

LUM_HUMAN STANDARD; PRT; 338 AA.

ID LUM_HUMAN

AC P51884; 0960M7;

DT 01-OCT-1996 (Rel. 34, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Luminan precursor (Keratan sulfate proteoglycan Luminan) (KSPG Luminan).

GN LUM OR LDC.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Cartilage, Intestine, and Placenta;

RX MEDLINE=95394964; PubMed=765616;

RA Grover J., Chen X.-N., Korenberg J.R., Roughley P.J.;

RT "The human Luminan gene. Organization, chromosomal location, and expression in articular cartilage."

RL J. Biol. Chem. 270:21942-21949(1995).

RN [2]

RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Cornea;

RX MEDLINE=9604734; PubMed=7558030;

RA Chakravarti S., Stallings R.L., Sundarraj N., Cornuet P.K., Hassell J.R.;

RT "Primary structure of human Luminan (Keratan sulfate proteoglycan) and localization of the gene (LUM) to chromosome 12q21.3-q22.1;"

RL Genomics 27:481-488(1995).

RN [3]

RN SEQUENCE FROM N.A.

CC TISSUE=Prostate; PubMed=12477932;
 CC MEDLINE=22388257;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.D., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallya S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- SUBUNIT: Binds to laminin (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix (By
 CC similarity).
 CC -1- TISSUE SPECIFICITY: Cornea and other tissues.
 CC -1- DEVELOPMENTAL STAGE: Present in the extracellular matrix of human
 CC articular cartilage at all ages, although its abundance is far
 CC greater in the adult. In the adult cartilage laminin exists
 CC predominantly in a glycoprotein form lacking keratan sulfate,
 CC whereas the juvenile form of the molecule is a proteoglycan.
 CC -1- SIMILARITY: BELONGS TO THE SMALL LEUCINE-RICH PROTEOGLYCAN
 CC (SLRP) FAMILY. CLASS II SUBFAMILY.
 CC -1- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: U18728; AAA85268.1; -
 CC EMBL: U21128; AAA91639.1; -
 CC EMBL: BC007038; AAH07038.1; -
 CC Genew: HGNC:6724; LUM.
 DR MIM: 600616; -
 DR GO: GO:0005578; C:extracellular matrix; TAS.
 DR GO: GO:0005203; F:proteoglycan; TAS.
 DR GO: GO:0007601; P:vision; TAS.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000372; LRR_Nterm.
 DR InterPro: IPR003551; LRR_Typ.
 DR Pfam: PF00560; LRR; 9.
 DR Pfam: PF01462; LRRNT; 1.
 DR PRINTS: PR00019; LEURICRPT.
 DR SMART: SMO0369; LRR_Typ; 1.
 DR SMART: SMO0013; LRRNT; 1.
 DR Glycoprotein; Extracellular matrix; Proteoglycan; Repeat;
 KW Leucine-rich repeat; Signal.
 FT CHAIN 1 18
 FT SIGNAL 1 18
 FT CHAIN 19 338
 FT DOMAIN 37 53
 FT REPEAT 59 76
 FT REPEAT 79 102
 FT REPEAT 103 128
 FT REPEAT 129 149
 FT REPEAT 150 171
 FT REPEAT 172 196
 FT REPEAT 197 217
 FT REPEAT 218 241
 FT REPEAT 242 266
 FT LRR-T 6.

FT REPEAT 267 286 LRR-S 4.
 FT REPEAT 287 316 LRR-T 7.
 FT REPEAT 317 338 LRR-T 8.
 FT DISULFID 295 328 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
 FT CARBOHYD 127 127 (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
 FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (KERATAN SULFATE)
 FT CARBOHYD 101 101 L -> P (IN REF. 1).
 FT CARBOHYD 101 101 L -> V (IN REF. 1).
 FT CARBOHYD 338 AA, 38429 MW, 90522BD370CC59D CRC64;
 SQ SEQUENCE
 Query Match 21.3%; Score 365.5; DB 1; Length 338;
 Best Local Similarity 32.0%; Pred. No. 7.5e-19;
 Matches 106; Conservative 57; Mismatches 135; Indels 33; Gaps 12;
 QY 13 DDDFEPRL-----GVCPPRCQC---HNAVQSDGLDKVPRDLPDPTLLDLONNKITE 65
 DB 22 DDFPLSTYGQSSPNCACBECNCPSPYPSAMTCDELKLSVPM-VPPGKYLYLRNNQIDH 80
 QY 66 IKDGFKNLKNLHALLIVNNKI--SKVSPGAFTPVVKLERLYLSKNQKELPEKPKPTIQ 123
 DB 81 IDKAFENVTDQWILDLNHLNLENSKIGKGRVPSKQKQKLIHNNNTLTSVGPLKSL 140
 QY 124 EIRAHENETTKRKVTENGDNOMVIELGTNPDKSSGIENGAFOQMKLSYRIADNTIT 183
 DB 141 DLQTLNNITKYG--SPGILVLTPIHQLHNLKEDAV-SAAFQKLSLEYLDLSFNQIA 197
 QY 164 SIPOGLPSPILHIDNKKISRYDAASIKGINNLAKGLSPFISANDN---GSLANTPH 240
 DB 198 RPSGLPVSLLTLTYLDNNKISNIPDEYFRFPAALOYLIRSHNELA--DSGLPNSFNVS 255
 QY 241 IREHLHNNKLTTRVPGGLAEHXYIOVYLIHNNNISVSSSDPCP---PGHNTKKSYSGV 297
 DB 256 LVELDLSYNKLNIP---TVNENLENYLLENVQLEKPKDKSKTLGPF-----LSYSKI 306
 QY 298 S---LPSNPVQYWEIQPSTPRCVYRSALIQ 325
 DB 307 KHLRLDGNRISSETSLPPDMYECLRVANREVT 337

Search completed: February 9, 2004, 11:36:34
 Job time : 29 secs

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OM protein - protein search, using sw model

Run on: February 9, 2004, 08:11:09 ; Search time 75 Seconds
(without alignments)
696.281 Million cell updates/sec

Title: US-10-004-176-6
Perfect score: 1713
Sequence: 1 VEAAGIGPEVDDRDPEPSL.....QPSTFRCVYRAAIQGNK 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1709	99.8	331	AA42260	
2	1709	99.8	331	AA42260	Mature decorin PT-
3	1709	99.8	331	AA42260	Human decorin amin
4	1709	99.8	331	AA42260	Human decorin amin
5	1709	99.8	331	AA42260	Novel central nerv
6	1709	99.8	331	AA42260	Collagen/decorin f
7	1704	99.5	342	AA42260	Amino acid sequenc
8	1653	96.5	353	AA42260	Human recombinant
9	1628	95.0	347	AA42260	Sequence of human
					Human decorin prot

10	1567	91.5	305	14	AA42267
11	1429	83.4	280	14	AA42266
12	1186	69.2	234	14	AA42265
13	985.5	57.5	359	16	AA87951
14	979	57.2	368	22	AA85043
15	979	57.2	368	24	AA839564
16	979	57.2	368	24	AA839564
17	979	57.2	368	24	AA839564
18	978.5	57.1	369	16	AA87952
19	976.5	57.0	332	16	AA87953
20	966	56.4	368	22	AA87951
21	965	56.3	368	11	AA80519
22	948	55.3	186	14	AA42264
23	943.5	55.1	379	21	AA801311
24	943.5	55.1	379	21	AA801311
25	943.5	55.1	379	23	AB895437
26	943.5	55.1	379	23	AB884831
27	943.5	55.1	379	24	ABU66733
28	943.5	55.1	379	24	ABU67009
29	943.5	55.1	379	24	ABU67121
30	943.5	55.1	379	24	ABU59814
31	943.5	55.1	379	24	ABU64916
32	943.5	55.1	379	24	ABU60230
33	943.5	55.1	379	24	ABU60341
34	943.5	55.1	379	24	ABU58350
35	943.5	55.1	379	24	ABU55920
36	943.5	55.1	379	24	ABU56301
37	943.5	55.1	379	24	ABU57236
38	943.5	55.1	379	24	ABU11302
39	941.5	55.0	379	22	AA440351
40	941.5	55.0	379	22	AA417820
41	927.5	54.1	332	22	ABG22569
42	925.5	54.0	373	23	AB805347
43	925.5	54.0	373	23	AB872356
44	742.5	43.3	423	22	AAU30348
45	735	42.9	146	20	AAV59749

ALIGNMENTS

RESULT 1	
AA42260	
ID	AA42260 standard; Protein; 331 AA.
XX	
AC	AA42260;
XX	
DT	25-MAR-2003 (updated)
DT	09-JAN-2003 (updated)
DT	28-APR-1994 (first entry)
XX	
DE	Mature decorin PT-65.
XX	
KW	leucine-rich repeat; proteoglycan; cell regulatory factor; MBP;
KW	fusion protein; maltose binding protein; tumour growth; inhibition;
KW	decorin; PG-II; PG-40; transforming growth factor-beta; TGF-beta.
XX	
OS	Bos sp.
XX	
PH	Key
FT	Region
FT	Region
FT	Region
FT	Region
FT	Region
XX	
PN	NO9320202-A1.
XX	
PD	14-OCT-1993.
XX	

Location/Qualifiers
1..45
/label= N-terminal region
/note="contains 4 Cys residues"
46..280
/label= repeat region
/note="contains 10 leucine-rich repeats"
281..331
/label= C-terminal region

PF 02-APR-1993; 93WO-US03171.
XX
XX 03-APR-1992; 92US-0865652.
XX
PA (LJOL-) LA JOLLA CANCER RES FOUND.
XX
PI Cardenas J, Craig W, Mullen DG, Pierschbacher MD;
XX PI Ruoslahti E;
XX
DR WPI: 1993-336910/42.
DR N-PSDB; AAQ50046.
XX
PT Active fragments of protein esp. decorin - with cell regulatory
PT factor domain, useful for inhibiting cell regulatory factor
PT activity
XX
PS Claim 10; Page 36-38; 77pp; English.
XX
CC Active fragments of decorin (full-length coding sequence AAQ50046)
CC were generated by PCR and fused to Maltose Binding Protein. The
CC resulting fusion proteins were useful for inhibiting the activity of
CC a cell regulatory factor, esp. TGF-beta, and hence for treating
CC conditions associated with over-activity of the growth factor such
CC as certain tumours.
CC (Updated on 09-JAN-2003 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 331 AA;
Query Match 99.8%; Score 1709; DB 14; Length 331;
Best Local Similarity 100.0%; Pred. No. 3.6e-145;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EASGIGPEVDDDDPEPSLGPVCPFRQCCHLRVQCSDGLDKVPKDLPPDTLLDLQNN 61
DB 4 EASGIGPEVDDDDPEPSLGPVCPFRQCCHLRVQCSDGLDKVPKDLPPDTLLDLQNN 63
QY 62 KITETKDGDFKLNKLNHALILVNNKISKVSPGAFPLVLELYLSKNOLEKELPEKMPKT 121
DB 64 KITETKDGDFKLNKLNHALILVNNKISKVSPGAFPLVLELYLSKNOLEKELPEKMPKT 123
QY 122 LOELRAHENEITKVRKVTENGKLNQMIYIELGTNPPLKSSGIENGAFQGMKKLSYIRIADTN 181
DB 124 LOELRAHENEITKVRKVTENGKLNQMIYIELGTNPPLKSSGIENGAFQGMKKLSYIRIADTN 183
QY 182 ITSIPQGLPPSLTEHLHDGKISRVDASLKGKLNIAKLGISFNSISAVNGSLANTPHL 241
DB 184 ITSIPQGLPPSLTEHLHDGKISRVDASLKGKLNIAKLGISFNSISAVNGSLANTPHL 243
QY 242 RELHLDNKKLTRVPGGLAEHKYIQVYLLHNNNISVVGSSDFCPGHNTKKAASYGVSLFS 301
DB 244 RELHLDNKKLTRVPGGLAEHKYIQVYLLHNNNISVVGSSDFCPGHNTKKAASYGVSLFS 303
QY 302 NPVOYWEIQPSTFRVCYVRSALQIGNYK 329
DB 304 NPVOYWEIQPSTFRVCYVRSALQIGNYK 331
RESULT 2
ID AA57079 standard; protein; 359 AA.
XX
XX AA57079;
XX
DT 28-FEB-2000 (first entry)
XX
XX Human decorin amino acid sequence.
XX
XX Neglected target tissue antigen; NTRA; autoimmunity; autoimmune response;
XX immunotherapeutic agent; insulin dependent diabetes mellitus;
XX multiple sclerosis; autoimmune thyroiditis; rheumatoid arthritis;
XX uveoretinitis; inflammatory response.
XX

OS Homo sapiens.
XX
XX MO9956763-A1.
XX
XX 11-NOV-1999.
XX
XX 07-MAY-1999; 99WO-US10250.
XX
XX 07-MAY-1998; 98US-0084636.
XX
XX (REGC) UNIT CALIFORNIA.
XX
XX Kaufman DL, Tian J, Olcott A;
XX
XX WPI: 2000-052905/04.
XX
PT Administration of neglected target tissue antigens to modulate immune
PT responses -
XX
XX Disclosure; Page 26; 79pp; English.
XX
XX Amino acid sequences AA57063-Y57091 are examples of neglected target
XX tissue antigens NTRA. NTRA are antigens (whole antigens or fragments)
XX not involved in autoimmunity. These peptides and proteins are used in
XX the method of the invention which involves administering an NTRA as an
XX antigen based immunotherapeutic agent, to a host afflicted with an
XX autoimmune response associated with an autoimmune disease. The
XX immunotherapeutic agent is used to treat autoimmune diseases such as
XX insulin dependent diabetes mellitus, multiple sclerosis, autoimmune
XX thyroiditis, uveoretinitis, rheumatoid arthritis or abnormal
XX inflammatory immune responses. The NTRA induces regulatory tolerance by
XX elicitation of regulatory T cells among T cells recognizing the NTRA but
XX not participating in the immune response. The NTRA are capable of
XX recognition by substantial populations of uncommitted T cells which can
XX be primed, or biased, towards regulatory responses to provide effective
XX treatment. The NTRA are effective in regulating undesirable immune
XX responses even when target determinants used as agents promoting
XX tolerance agents have failed to induce an effective regulatory T cell
XX response. NTRA as agents promoting tolerance are anticipated to be safer
XX than use of target determinants.
XX
SQ Sequence 359 AA;
Query Match 99.8%; Score 1709; DB 21; Length 359;
Best Local Similarity 100.0%; Pred. No. 4e-145;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EASGIGPEVDDDDPEPSLGPVCPFRQCCHLRVQCSDGLDKVPKDLPPDTLLDLQNN 61
DB 32 EASGIGPEVDDDDPEPSLGPVCPFRQCCHLRVQCSDGLDKVPKDLPPDTLLDLQNN 91
QY 62 KITETKDGDFKLNKLNHALILVNNKISKVSPGAFPLVLELYLSKNOLEKELPEKMPKT 121
DB 92 KITETKDGDFKLNKLNHALILVNNKISKVSPGAFPLVLELYLSKNOLEKELPEKMPKT 151
QY 122 LOELRAHENEITKVRKVTENGKLNQMIYIELGTNPPLKSSGIENGAFQGMKKLSYIRIADTN 181
DB 152 LOELRAHENEITKVRKVTENGKLNQMIYIELGTNPPLKSSGIENGAFQGMKKLSYIRIADTN 211
QY 182 ITSIPQGLPPSLTEHLHDGKISRVDASLKGKLNIAKLGISFNSISAVNGSLANTPHL 241
DB 212 ITSIPQGLPPSLTEHLHDGKISRVDASLKGKLNIAKLGISFNSISAVNGSLANTPHL 271
QY 242 RELHLDNKKLTRVPGGLAEHKYIQVYLLHNNNISVVGSSDFCPGHNTKKAASYGVSLFS 301
DB 272 RELHLDNKKLTRVPGGLAEHKYIQVYLLHNNNISVVGSSDFCPGHNTKKAASYGVSLFS 331
QY 302 NPVOYWEIQPSTFRVCYVRSALQIGNYK 329
DB 332 NPVOYWEIQPSTFRVCYVRSALQIGNYK 359
RESULT 3

ID	AAG78511
AC	AAG78511 standard; protein; 359 AA.
XX	
XX	AAG78511;
DT	29-JAN-2002 (first entry)
XX	
DE	Human decorin amino acid sequence.
KW	Fibromodulin; Decorin; Biglycan; Proteoglycan; Extracellular matrix; TGF-beta; Transforming growth factor-beta; Burn, Wound; Cytostatic; Nephrotropic; Antithematic; Antiarthritic; Vasotrophic; Vulnary Antiarteriosclerotic; Hepatotropic; Cardiant; Dermatological; Glomerulonephritis; Rheumatoid arthritis; Arteriosclerosis; Adult respiratory distress syndrome; Cirrhosis; Cancer; Fibrotic.
KM	
XX	
OS	Homo sapiens.
FT	
FT	Key Location/Qualifiers
FT	Peptide 1..30
FT	/label= Signal_peptide
FT	Protein 31..359
FT	/label= Mature_human_decorin
PN	US6277812-B1.
XX	
PD	21-AUG-2001.
XX	
PF	02-JUN-1995; 95US-0458834.
XX	
PR	14-NOV-1991; 91US-0792192. 17-NOV-1992; 92US-0978931. 08-SEP-1994; 94US-0303238. 28-JUN-1988; 88US-0212702. 22-JAN-1990; 90US-0467888. 13-MAY-1992; 92US-0882345.
PR	
XX	(BURN-) BURNHAM INST.
PA	
XX	Ruoslahti EI, Yamaguchi Y;
PI	WPI; 2001-610491/70.
DR	
XX	
PT	Use of decorin or biglycan polypeptide for inhibiting TGF-beta activity in the treatment of dermal wounds and cancer -
PS	Example 8; Fig 11; 40pp; English.
CC	The invention relates to the inhibition of transforming growth factor-beta (TGF-beta) actively involving contacting TGF-beta with a purified polypeptide comprising leucine-rich amino acid sequence of a member of decorin superfamily of mammalian proteoglycans. The following activities can be attributed to the polypeptide of the invention: cytostatic, nephrotropic, antirheumatic, antiarthritic, vasotropic, antiarteriosclerotic, hepatotropic, cardiant, dermatological and vulnary. Polypeptides of the invention act as transforming growth factor-beta (TGF-beta) binder. The polypeptides of the invention can be used for treating a pathology, particularly proliferative pathology caused by a transforming growth factor-beta (TGF-beta) regulated activity such as cancer; particularly fibrotic cancer, fibrotic disease, glomerulonephritis, rheumatoid arthritis, arteriosclerosis, adult respiratory distress syndrome, cirrhosis of liver, fibrosis of lungs, post-myocardial infarction, cardiac fibrosis, post-angioplasty restenosis, renal interstitial fibrosis and certain dermal fibrotic conditions such as keloids and scarring resulting from burn injuries; other invasive skin injuries and reconstructive surgery. The wounds treated with the polypeptide, particularly decorin exhibit no detectable scarring, and are histologically normal. The current sequence represents human decorin.
CC	
XX	
SQ	Sequence 359 AA;

Query Match 99.8%; Score 1709; DB 22; Length 359;

	Best Local Similarity	100.0%;	Pred. No. 4e-145;	
	Matches	328;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	2	EASGIGEVDPDDRRFEPSPGLPVCEPFRCCCHLRVOCSDLGIDKVPKDLPDPTLLDLQNN	61	
Dd	32	EASGIGEVDPDDRRFEPSPGLPVCEPFRCCCHLRVVQCSDLGIDKVPKDLPDPTLLDLQNN	91	
QY	62	KITEIKGDGFKNLKNTHALLLVNKKISKVSPPGAFTPLVKLERLYLSKQULKELPEKMPKT	121	
Dd	92	KITEIKGDGFKNLKNTHALLLVNKKISKVSPPGAFTPLVKLERLYLSKQULKELPEKMPKT	151	
QY	122	LOEIRAHENETTKRKATFENGLOMTYIEIGTPMLKSSGIENGAFQGMKKLSYRIADTN	181	
Dd	152	LOEIRAHENETTKRKATFENGLOMTYIEIGTPMLKSSGIENGAFQGMKKLSYRIADTN	211	
QY	182	ITSIPQGLPSPLTEHLDDGNKISRVDAAISKLGINLNAKLGISFNISIAVDNGSLANTPHL	241	
Dd	212	ITSIPQGLPSPLTEHLDDGNKISRVDAAISKLGINLNAKLGISFNISIAVDNGSLANTPHL	271	
QY	242	RELHLDNNKLTTRVPGSLAEHKYIOVYLHNNTISVGSSDPCPGPHNTTKKASYSGVSLFS	301	
Dd	272	RELHLDNNKLTTRVPGSLAEHKYIOVYLHNNTISVGSSDPCPGPHNTTKKASYSGVSLFS	331	
QY	302	NPQVWEIOPSTFRFCVVRSAIQGNKYK	329	
Dd	332	NPQVWEIOPSTFRFCVVRSAIQGNKYK	359	
RESULT 4				
AU087286	ID	AU087286 standard; Protein; 360 AA.		
XX	AC	AU087286;		
XX	DT	05-JUN-2002 (first entry)		
DE		Novel central nervous system protein #196.		
XX				
KM		Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;		
KW		hyperproliferative disorder; neoplasia; cardiovascular disorder;		
KM		cardiac arrest; cerebrovascular disorder; ischemia; angiogenesis;		
KM		nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;		
KM		acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;		
KM		adenocarcinoma; reproductive system disorder; testicular feminisation;		
KM		endocrine disorder; diabetes; cancer; leukemia; neovascularization;		
KM		respiratory disorder; renal disorder; kidney failure; blood disorder;		
KM		myocardial infarction; wound healing; cell proliferation; skin aging;		
KM		food additive; food preservative; gene therapy.		
OS		Homo sapiens.		
XX				
PN		WO200155318-A2.		
XX				
PF		02-AUG-2001.		
XX				
XX		17-JAN-2001; 2001WO-US01332.		
PR				
XX				
PR	31-JAN-2000;	2000US-0179065.		
PR	04-FEB-2000;	2000US-0180628.		
PR	24-FEB-2000;	2000US-0184664.		
PR	02-MAR-2000;	2000US-0186350.		
PR	16-MAR-2000;	2000US-0189874.		
PR	17-MAR-2000;	2000US-0190076.		
PR	18-APR-2000;	2000US-0198123.		
PR	19-MAY-2000;	2000US-0205515.		
PR	07-JUN-2000;	2000US-0209467.		
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 PR 14-AUG-2000; 2000US-0224519.
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 PR 14-AUG-2000; 2000US-0225266.
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 PR 22-AUG-2000; 2000US-0226681.
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 PR 23-AUG-2000; 2000US-0227187.
 PR 30-AUG-2000; 2000US-0227009.
 PR 01-SEP-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
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 PR 05-SEP-2000; 2000US-0229509.
 PR 06-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 08-SEP-2000; 2000US-0231243.
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 PR 08-SEP-2000; 2000US-0232080.
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 PR 20-OCT-2000; 2000US-0240960.
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 PR 01-NOV-2000; 2000US-0241826.
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 PR 08-NOV-2000; 2000US-0244674.

PR 08-NOV-2000; 2000US-0246475.
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 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
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 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI: 2001-581633/65.
 N-PSDB; ABR43616.
 XX
 PT New isolated nucleic acid encoding a protein for diagnosing,
 PT preventing, treating or ameliorating medical conditions and used as
 PT food additives or preservatives -
 XX
 PS Claim 9; SEQ ID No 804; 837pp; English.
 XX
 CC The invention describes an isolated nucleic acid molecule (I) encoding a
 CC novel central nervous system protein. (I) and polypeptides (II) encoded
 CC by (I), are used to treat a medical conditions and in diagnosis of a
 CC pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia,
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and
 CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses
 CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
 CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,
 CC adenocarcinomas and irritable bowel syndrome, reproductive system

disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,

Query Match 99.8%; Score 1709; DB 22; Length 360;

Best Local Similarity 100.0%; Pred. No. 4e-145; Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDRDPEPSLGVPVPCPCQCHLRVQCSDGLDVKVPDLPDPTLLDLQNN 61
DB 33 EASGIGPEVDDRDPEPSLGVPVPCPCQCHLRVQCSDGLDVKVPDLPDPTLLDLQNN 92
QY 62 KITETKDGDFKNNKNTLHLLVNNKISKVSPGAFPLVKLERLYLSKNOLKEPEKMPKT 121
DB 93 KITETKDGDFKNNKNTLHLLVNNKISKVSPGAFPLVKLERLYLSKNOLKEPEKMPKT 152
QY 122 LQELRAHENEITVRKVTENGNNQIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN 181
DB 153 LQELRAHENEITVRKVTENGNNQIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN 212
QY 182 ITSIPQGLPPSLTEHLHDGKISRVDASIKGINLAKLGLSTNSISAVDNGSLANTPHL 241
DB 213 ITSIPQGLPPSLTEHLHDGKISRVDASIKGINLAKLGLSTNSISAVDNGSLANTPHL 272
QY 242 RELHLNNKLTTRPGGLAEHKYIQVYVLLHNNNISVVGSSDPFCPPGHNTKASYSGLSFS 301
DB 273 RELHLNNKLTTRPGGLAEHKYIQVYVLLHNNNISVVGSSDPFCPPGHNTKASYSGLSFS 332
QY 302 NPQVWEIQPSTFRVCYVRSALQIGNYK 329
DB 333 NPQVWEIQPSTFRVCYVRSALQIGNYK 360

RESULT 5
AAR89471
ID AAR89471 standard; Protein; 1388 AA.

XX AAR89471;

XX 01-OCT-1996 (first entry)

XX Collagen/decortin fusion protein.

KW Transforming growth factor; TGF-beta-1; collagen IA; osteogenesis;
KM bone formation; tissue repair; fusion protein.

XX Synthetic.

XX Key location/Qualifiers

FT Domain 1..1057
FT /label= Collagen-IA
FT /note= "collagen IA alpha-helical domain"

FT Peptide 1058..1059
FT /label= linker_peptide

FT Domain 1060..1388
FT /label= Decorin

FT Misc-difference 887
FT /note= "unidentified amino acid"

FT Misc-difference 890
FT /note= "unidentified amino acid"

XX CA2151547-A.

XX 11-DGC-1995.

PF 12-JUN-1995; 95CA-2151547.

XX 10-JUN-1994; 94US-0259263.

XX (USSU) US SURGICAL CORP.

XX Espino P, Gruskin EA;

XX WPI; 1996-140144/15.

DR N-PSDB; AAT16517.

XX Chimeric DNA encoding protein contg. extracellular matrix protein

PT domain - and cellular regulatory factor domain, partic. useful as

PT osteogenic agents; also related vectors, transformed cells and

XX chimeric proteins.

XX Disclosure; Fig 7; 59pp; English.

XX A fusion protein (AAR89471) comprises the alpha-helical region of

CC human collagen I(a) linked to human dermal sulphate proteoglycan

CC (decorin). It can be expressed in Escherichia coli transformants

CC carrying a vector incorporating a chimeric gene (AAT16517) coding for

CC the fusion. The decorin binds to type I collagen and thus affects

CC fibrin formation. It inhibits the cell attachment-promoting

CC activity of collagen and fibrinogen by binding to such molecules

CC near their cell binding sites. The collagen moiety provides an

CC integral substratum or scaffolding for the decorin. The fusion

XX protein acts to reduce scarring of healing tissue.

XX Sequence 1388 AA;

XX Query Match 99.8%; Score 1709; DB 17; Length 1388;

XX Best Local Similarity 100.0%; Pred. No. 2.9e-144;

XX Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDRDPEPSLGVPVPCPCQCHLRVQCSDGLDVKVPDLPDPTLLDLQNN 61

DB 1061 EASGIGPEVDDRDPEPSLGVPVPCPCQCHLRVQCSDGLDVKVPDLPDPTLLDLQNN 1120

QY 62 KITETKDGDFKNNKNTLHLLVNNKISKVSPGAFPLVKLERLYLSKNOLKEPEKMPKT 121

DB 1121 KITETKDGDFKNNKNTLHLLVNNKISKVSPGAFPLVKLERLYLSKNOLKEPEKMPKT 1180

QY 122 LQELRAHENEITVRKVTENGNNQIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN 181

DB 1181 LQELRAHENEITVRKVTENGNNQIVIELGTNPLKSSGIENGAFQGMKKLSYIRIADTN 1240

QY 182 ITSIPQGLPPSLTEHLHDGKISRVDASIKGINLAKLGLSTNSISAVDNGSLANTPHL 241

DB 1241 ITSIPQGLPPSLTEHLHDGKISRVDASIKGINLAKLGLSTNSISAVDNGSLANTPHL 1300

QY 242 RELHLNNKLTTRPGGLAEHKYIQVYVLLHNNNISVVGSSDPFCPPGHNTKASYSGLSFS 301

DB 1301 RELHLNNKLTTRPGGLAEHKYIQVYVLLHNNNISVVGSSDPFCPPGHNTKASYSGLSFS 1360

QY 302 NPQVWEIQPSTFRVCYVRSALQIGNYK 329

DB 1361 NPQVWEIQPSTFRVCYVRSALQIGNYK 1388

RESULT 6
AAV84539
ID AAV84539 standard; Protein; 1388 AA.

XX AAV84539;

XX 25-JUL-2000 (first entry)

XX Amino acid sequence of a chimeric collagen 1 (alpha1)/decorin protein.

XX Extracellular matrix protein; self aggregation; hydroxylated proline;

KW trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production;

KM collagen; fibrinogen; fibronectin; post translational hydroxylation;

CC Human recombinant decorin (AAR89439) was obtd. by expression of a
CC cDNA clone (AA110741) in CHO host cells. Decorin (or PGII or PG-40)
CC is a proteoglycan having a 40 kDa core protein. Recombinant
CC decorin can be produced by cotransfection of CHO-DG4 cells with
CC pSV2-decorin and pSV4ohfr. Large-scale cultures can be performed
CC using CHO cells attached to microcarrier beads. The recombinant
CC protein is purified from the cells using a 3-step chromatographic
CC procedure. It can be used for the highly sensitive detection of
CC guanidinium ions (ppm range), partic. in protein-contg. solns.
CC purified using GuHCl, and also has therapeutic applns.

XX Sequence 342 AA;

Query Match 99.5%; Score 1704; DB 17; Length 342;
Best Local Similarity 100.0%; Pred. No. 1,1e-144;

Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDRDPEPSLGPVCPFRQCHLRVVOCSDLGLDKVPKDLPPDTLLDLQNN 61

DB 16 EASGIGPEVDDRDPEPSLGPVCPFRQCHLRVVOCSDLGLDKVPKDLPPDTLLDLQNN 75

QY 62 KITTEIKDGFKNLKNHALILVNNKISKVSPGAFPLVTLERLYLSKNQKELPEKMPKT 121

DB 76 KITTEIKDGFKNLKNHALILVNNKISKVSPGAFPLVTLERLYLSKNQKELPEKMPKT 135

QY 122 LOELRAHENEITKVRKVTENGNGMIVIELGTNPLKSSGGENGAFOGKKLSYIRIADTN 181

DB 136 LOELRAHENEITKVRKVTENGNGMIVIELGTNPLKSSGGENGAFOGKKLSYIRIADTN 195

QY 182 ITSIPQGLPSSLTELHLDGNKISRVDASLKGNNLAKGLSFNSISAVDNGSLANTPHL 241

DB 196 ITSIPQGLPSSLTELHLDGNKISRVDASLKGNNLAKGLSFNSISAVDNGSLANTPHL 255

QY 242 RELHLDNNKLTTRVPGGLAEHKYIQVYLLHNNNISVVGSSDFCPGHNTKKAASYGSLFS 301

DB 256 RELHLDNNKLTTRVPGGLAEHKYIQVYLLHNNNISVVGSSDFCPGHNTKKAASYGSLFS 315

QY 302 NPVOYWEIOPSTFRCYVRSALQIGNY 328

DB 316 NPVOYWEIOPSTFRCYVRSALQIGNY 342

RESULT 8

AAR05160 standard; protein; 353 AA.

AC AAR05160;

DT 25-MAR-2003 (updated)

DT 17-DEC-2001 (updated)

DT 09-OCT-1990 (first entry)

DE Sequence of human bone proteoglycan II (decorin).

XX Osteoporosis; rheumatoid arthritis; Paget's disease;

KM atherosclerosis; periodontal; human bone matrix; proteoglycan.

XX Homo sapiens.

XX USN7432044-N.

XX 17-APR-1990.

XX 03-NOV-1989; 89US-0142159.

XX 03-NOV-1989; 89US-0142159.

XX (USSH) NAT INST OF HEALTH.

XX Termine J;

XX WPI; 1990-178641/23.

DR N-PSDB; AA004491.

XX Human bone matrix DNA and proteins -
PT used in detection, diagnosis and treatment involving skeletal
PT and/or connective tissue disease states.

PS Disclosure; Page ?; ?pp; English.

XX Probes and Abs raised to the proteins can be used to determine

CC their levels useful in diagnosis of associated connective tissue

CC diseases states such as osteoporosis, osteo/rheumatoid arthritis,

CC Paget's disease, atherosclerosis and periodontal disease.

CC Proteins may also be used to induce or block biological function.

CC (Note: Revised entry submitted to correct the patent number format of

CC US Government-owned NTIS applications to prevent clashes with ongoing US

CC granted patent numbers. For further information please visit the Derwent

CC web site at www.derwent.com/dmpi/updates/ntis_us.html.)

CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 353 AA;

Query Match 96.5%; Score 1653; DB 11; Length 353;
Best Local Similarity 97.3%; Pred. No. 4.3e-140;

Matches 319; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDRDPEPSLGPVCPFRQCHLRVVOCSDLGLDKVPKDLPPDTLLDLQNN 61

DB 26 EASGIGPEVDDRDPEPSLGPVCPFRQCHLRVVOCSDLGLDKVPKDLPPDTLLDLQNN 85

QY 62 KITTEIKDGFKNLKNHALILVNNKISKVSPGAFPLVTLERLYLSKNQKELPEKMPKT 121

DB 86 KITTEIKDGFKNLKNHALILVNNKISKVSPGAFPLVTLERLYLSKNQKELPEKMPKT 145

QY 122 LOELRAHENEITKVRKVTENGNGMIVIELGTNPLKSSGGENGAFOGKKLSYIRIADTN 181

DB 146 LOELRAHENEITKVRKVTENGNGMIVIELGTNPLKSSGGENGAFOGKKLSYIRIADTN 205

QY 182 ITSIPQGLPSSLTELHLDGNKISRVDASLKGNNLAKGLSFNSISAVDNGSLANTPHL 241

DB 206 ITSIPQGLPSSLTELHLDGNKISRVDASLKGNNLAKGLSFNSISAVDNGSLANTPHL 265

QY 242 RELHLDNNKLTTRVPGGLAEHKYIQVYLLHNNNISVVGSSDFCPGHNTKKAASYGSLFS 301

DB 266 RELHLDNNKLTTRVPGGLAEHKYIQVYLLHNNNISVVGSSDFCPGHNTKKAASYGSLFS 325

QY 302 NPVOYWEIOPSTFRCYVRSALQIGNY 329

DB 326 NPVOYWEIOPSTFRCYVRSALQIGNY 353

RESULT 9

AAE34392 standard; Protein; 347 AA.

AC AAE34392;

DT 14-MAY-2003 (first entry)

XX Human decorin protein.

XX Human, diagnosis; osteoarthritis; rheumatoid arthritis; decorin.

XX Homo sapiens.

XX WO200295415-A2.

XX 28-NOV-2002.

XX 22-MAY-2002; 2002WO-EP05612.

XX 23-MAY-2001; 2001GB-0012626.

XX (OSTE-) OSTEO-METER BIO TECH AS.

XX Christgau S, Henriksen DB, Cloos PAC,
XX WPI; 2003-140389/13.
XX
XX An assay for the diagnosis or assessment of the severity of
PT osteoarthritis or rheumatoid arthritis comprising detecting an
PT isomerized or optically inverted protein in a sample -
XX
XX Disclosure; Page 68-70; 106pp; English.
XX
XX The invention relates to an assay for the diagnosis or assessment of
CC the severity of osteoarthritis or rheumatoid arthritis. The assay
CC involves measuring (in a biological sample) the amount or presence of
CC an isomerized or optically inverted protein or one or more isomerized
CC or optically inverted fragments from proteins such as perlecan,
CC biglycan, decorin, fibrillin-1 or procadherin. The assay is useful
CC for the diagnosis or assessment of the severity of osteoarthritis or
CC rheumatoid arthritis. The present sequence is human decorin protein.
XX
XX Sequence 347 AA;
SQ
Query Match 95.0%; Score 1628; DB 24; Length 347;
Best Local Similarity 96.3%; Pred. No. 7,4e-138;
Matches 316; Conservative 0; Mismatches 0; Indels 12; Gaps 1;
XX
QY 2 EASGIGEPVDDRDPEPSLGPVCPFCRCQCHLRVQCSDLGLDKVPKDLPPDTLLDLQNN 61
DB |||||
32 EASGIGEPVDDRDPEPSLGPVCPFCRCQCHLRVQCSDLGLDKVPKDLPPDTLLDLQNN 91
QY KITEIKDGPKNLKNLHALLVNNKISKVSPGATPLVLERLYLSKNQKELPERKPKT 121
DB |||||
92 KITEIKDGPKNLKNLHALLVNNKISKVSPGATPLVLERLYLSKNQKELPERKPKT 151
QY 122 LOELRAHEHEITKRVKATFNGLNQMTVIELGTNPPLKSSGIEENGAFQGMKKLSYIRADTN 181
DB |||||
152 LOELRAHEHEITKRVKATFNGLNQMTVIELGTNPPLKSSGIEENGAFQGMKKLSYIRADTN 211
QY 182 ITSIPQGLPSSLTEHLHDGNNKISRVDASLKGANNLAKGLSFNSISAVDNGSLANTPHL 241
DB |||||
212 ITSIPQGLPSSLTEHLHDGNNKISRVDASLKGANNLAKGLSFNSISAVDNGSLANTPHL 271
QY 242 RELHLDNNKLTTRVPGGLAEHKYIQVYVLLHNNNISVVGSSDFPCPGHNTKKAASYSGVSLFS 301
DB |||||
272 RELHLDNNKLTTRVPGGLAEHKYIQVYVLLHNNNISVVGSSDFPCPGHNTKKAASYSGVSLFS 319
QY 302 NPVOYWEIOPSTFRVCYVRSALIQGNKY 329
DB |||||
320 NPVOYWEIOPSTFRVCYVRSALIQGNKY 347

RESULT 10
AAR42267
ID AAR42267 standard; Protein; 305 AA.
XX
AC AAR42267;
XX
DT 25-MAR-2003 (updated)
DT 09-JAN-2003 (updated)
DT 28-APR-1994 (first entry)
XX
DE Decorin sequence PT-78 (N-terminal to half C-terminal).
XX
XX leucine-rich repeat; proteoglycan; cell regulatory factor; MBP;
KM fusion protein; maltose binding protein; tumour growth; inhibition;
KM decorin; PG-II; PG-40; transforming growth factor-beta; TGF-beta.
XX
OS Bos sp.
XX
XX WO9320202-A1.
XX
XX 14-OCT-1993.
XX

PF 02-APR-1993; 93MO-US03171.
XX
XX 03-APR-1992; 92US-0865652.
XX
XX (JOL-) LA JOLLA CANCER RES FOUND.
PA
XX Cardenas J, Craig W, Mullen DG, Pierschbacher MD;
PI Rosenthal E;
XX
XX WPI; 1993-336910/42.
DR N-PSDB; AAQ50053.
XX
XX
PT Active fragments of decorin esp. decorin - with cell regulatory
PT factor domain, useful for inhibiting cell regulatory factor
PT activity
XX
PS Claim 10; Page 49-50; 77pp; English.
XX
XX Active fragments of decorin (full-length coding sequence AAQ50046)
CC were generated by PCR and fused to Maltose Binding Protein. The
CC resulting fusion proteins were useful for inhibiting the activity of
CC a cell regulatory factor, esp. TGF-beta, and hence for treating
CC conditions associated with over-activity of the growth factor such
CC as certain tumours
CC (Updated on 09-JAN-2003 to add missing OS field.)
CC
SQ Sequence 305 AA;
Query Match 91.5%; Score 1567; DB 14; Length 305;
Best Local Similarity 100.0%; Pred. No. 1.9e-132;
Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2 EASGIGEPVDDRDPEPSLGPVCPFCRCQCHLRVQCSDLGLDKVPKDLPPDTLLDLQNN 61
DB |||||
4 EASGIGEPVDDRDPEPSLGPVCPFCRCQCHLRVQCSDLGLDKVPKDLPPDTLLDLQNN 63
QY 62 KITEIKDGPKNLKNLHALLVNNKISKVSPGATPLVLERLYLSKNQKELPERKPKT 121
DB |||||
64 KITEIKDGPKNLKNLHALLVNNKISKVSPGATPLVLERLYLSKNQKELPERKPKT 123
QY 122 LOELRAHEHEITKRVKATFNGLNQMTVIELGTNPPLKSSGIEENGAFQGMKKLSYIRADTN 181
DB |||||
124 LOELRAHEHEITKRVKATFNGLNQMTVIELGTNPPLKSSGIEENGAFQGMKKLSYIRADTN 183
QY 182 ITSIPQGLPSSLTEHLHDGNNKISRVDASLKGANNLAKGLSFNSISAVDNGSLANTPHL 241
DB |||||
184 ITSIPQGLPSSLTEHLHDGNNKISRVDASLKGANNLAKGLSFNSISAVDNGSLANTPHL 243
QY 242 RELHLDNNKLTTRVPGGLAEHKYIQVYVLLHNNNISVVGSSDFPCPGHNTKKAASYSGVSLFS 301
DB |||||
244 RELHLDNNKLTTRVPGGLAEHKYIQVYVLLHNNNISVVGSSDFPCPGHNTKKAASYSGVSLFS 303
QY 302 NP 303
DB |||||
304 NP 305

RESULT 11
AAR42266
ID AAR42266 standard; Protein; 280 AA.
XX
AC AAR42266;
XX
DT 25-MAR-2003 (updated)
DT 09-JAN-2003 (updated)
DT 28-APR-1994 (first entry)
XX
DE Decorin sequence PT-77 (N-terminal to LRRI0).
XX
XX leucine-rich repeat; proteoglycan; cell regulatory factor; MBP;
KM fusion protein; maltose binding protein; tumour growth; inhibition;
KM decorin; PG-II; PG-40; transforming growth factor-beta; TGF-beta.
XX


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XX OS Rattus sp.
XX Key Location/Qualifiers
XX FT Peptide 1..37
XX FT /label= Sig_peptide
XX FT Region 44..60
XX FT /label= Hypervariable_region
XX PN MO9530432-A1.
XX 16-NOV-1995.
XX PD 09-MAY-1994; 94MO-EP01479.
XX PR 09-MAY-1994; 94MO-EP01479.
XX PR (BOBF) BOEHRINGER MANNHEIM GMBH.
XX PI Haeneohl R, Huston J, Jungmans U, Kappler J, Koops A,
XX PI Mueller HW;
XX DR WPI: 1995-403938/51.
XX DR N-PSDB; AAT08768.
XX PT Proteoglycan cpds., partic. chondroitin sulphate proteoglycan(s) -
XX PT for maintain structural and function of the CNS and attenuating
XX PT memory deficit(s) in the elderly and patients with dementia
XX PS Claim 1; Page 44-45; 60pp; English.
XX CC Rat biglycan (AAR87951) is a chondroitin sulphate proteoglycan with
XX CC neurotrophic activity for brain neurons. Recombinant biglycan,
XX CC obd., by expression of encoding cDNA (AAT08768) in eukaryotic host
XX CC cells, can be used to enhance the survival and maintain the structure
XX CC and function of CNS neurons during normal ageing as well as after
XX CC pathological and/or traumatic nervous system damage. It can also
XX CC be used to restore function following nervous system lesions and
XX CC degenerative diseases, and to improve learning efficiency and memory
XX CC in the elderly and in patients with dementia.
XX SQ Sequence 369 AA;

Query Match 57.5%; Score 985.5; DB 16; Length 369;
Best Local Similarity 57.6%; Pred. No. 5.2e-80;
Matches 190; Conservative 51; Mismatches 86; Indels 3; Gaps 2;

QY 2 EASGIGPE--VPDRDFEPSLGPVCFRCOCHLRVVOCSDLGLKVPKDLPPDTLLDLQ 59
DB 40 EASGDTTSGVVDLSDLTPTFSAMCPFGCHCHLRVVOCSDLGLKVPKDISPDTLLDLQ 99
QY 60 NNTKTEIKDGPDKNLKNAHLILVNNKISKVSPGAFPLVLERLYLSKNQKELPEKMP 119
DB 100 NNDISELRKDPFKGLQHLIYALVIVNNKISKIHEKAFSLRLQKLYISKNLVLEIPMP 159
QY 120 KTLQELRAHENEITYKRVKTNGNLQMTVIELGTNPILKSSGIENGAFQGMKGLSYIRIAD 179
DB 160 SSLVELRIHDNRIRKVPKGVFSGLRNMNCIEMGNGPLNENSGFEPAFDGL-KLNYLRISR 218
QY 180 TNITISPGGLPPLSLTELHLDNKISRVAASLKLGNLNLAKIGLSNNGISAVDNGLATNP 239
DB 219 AKLTGIPDLPETLDELHLDNKIQALEDLIRYSKYLRLGLGNQIRMTENGLSLFLP 278
QY 240 HLRRLHLDNNKLTLPVPGGLAEHKYIQVYLLHNNNISVVGSSDFCPGHNTKKASVGSVL 299
DB 279 TLRELHLDNNKLTSLVPAGLPLKLLQVYLLHNNNISNNTKGINDFCMGCVGRATYNGISL 338
QY 300 FSNFVQWEIOPSTFRVCYVRSATQLGNK 329
DB 339 FNNFVPMWEVQPAFRVCYVRLAQLQFGNKK 368

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AAB85043
ID AAB85043 standard; Protein; 368 AA.
XX AC AAB85043;
XX AC AAB85043;
XX DT 06-AUG-2001 (first entry)
XX DE Human biglycan protein sequence.
XX KM Dystrophin-associated protein complex; DAPC; postsynaptic membrane;
XX KM biglycan; muscular dystrophy; neuromuscular; neurological; smooth muscle;
XX KM nootropic; neuroleptic; antiviral.
XX OS Homo sapiens.
XX PN MO200136475-A2.
XX PD 25-MAY-2001.
XX PR 17-NOV-2000; 2000MO-US31661.
XX PR 18-NOV-1999; 99US-0166253.
XX PR (UTBR-) UNIV BROWN RES FOUND.
XX PI Fallon J, McKechnie B, Rafil M, Creely H, Bowe M, Ferri R;
XX PI WPI: 2001-355617/37.
XX DR N-PSDB; AAF83977.
XX PT Stabilizing dystrophin-associated protein complexes and activating
XX PT postsynaptic membrane of a cell for treating or preventing muscular,
XX PT neuromuscular and neurological disorders, involves contacting cell with
XX PT biglycan -
XX PS Disclosure; Page 101-108; 112pp; English.
XX CC The invention relates to stabilizing dystrophin-associated protein
XX CC complexes (DAPCs) on the surface of a cell or activating a postsynaptic
XX CC membrane of a cell that comprises contacting the cell with an effective
XX CC amount of biglycan. A composition comprising biglycan or its portion
XX CC is useful for treating or preventing a condition associated with abnormal
XX CC DAPC in cells, characterized by breakdown of muscle cell membrane, which
XX CC includes muscular dystrophies, such as Duchenne's, Becker's, Congenital,
XX CC limb-girdle muscular dystrophy and myotonic dystrophy and a condition
XX CC characterized by abnormal neuromuscular junction or synapse, such as
XX CC neuromuscular or neurological diseases in a subject. Neurological
XX CC disorders, include polymyositis and Alzheimer's disease. Biglycan is also
XX CC useful for preventing and treating smooth muscle disorders, such as
XX CC cardiac myopathies and for treating and inhibiting infections of cells by
XX CC microorganisms e.g. viruses. Agents that modulate the activity of
XX CC DAC-125, identified by the methods are useful in the prophylactic and
XX CC therapeutic treatments of diseases or disorders, characterized by an
XX CC unstable DAPC or an inappropriate formation of a postsynaptic
XX CC differentiation. Biglycans are also useful as a supplement to brain or
XX CC muscle cell or tissue culture and, tissues can be incubated in vitro
XX CC with biglycan to reverse tissue atrophy and to improve their growth or
XX CC survival in vitro. The present sequence represents the human biglycan.
XX SQ Sequence 368 AA;

Query Match 57.2%; Score 979; DB 22; Length 368;
Best Local Similarity 57.4%; Pred. No. 2e-79;
Matches 189; Conservative 50; Mismatches 88; Indels 2; Gaps 2;

QY 2 EASGIGPE--VPDRDFEPSLGPVCFRCOCHLRVVOCSDLGLKVPKDLPPDTLLDLQ 60
DB 40 EASGADTSGVLDPSVTPYTSAMCPFGCHCHLRVVOCSDLGLKVPKDISPDTLLDLQ 99
QY 61 NNTKTEIKDGPDKNLKNAHLILVNNKISKVSPGAFPLVLERLYLSKNQKELPEKMP 120
DB 100 NDISELKDPFKGLQHLIYALVIVNNKISKIHEKAFSLRLQKLYISKNLVLEIPMP 159

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CC The present invention describes a method for assessing whether a patient
CC is afflicted with breast cancer. The method comprises comparing the level
CC of expression of a marker (gene/polypeptide see ACCS0076 to ACCS0334 and
CC ABR736 to ABR47632) in a patient sample and the normal level of
CC expression of the marker in a control non-breast cancer sample, where a
CC significant increase in the level of expression of the marker in the
CC patient sample and the normal level is an indication that the patient is
CC afflicted with breast cancer. The breast cancer associated sequences
CC from the present invention have cytosolic activities and can be used in
CC gene therapy. The method is useful for diagnosing and treating breast
CC cancer.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 368 AA;

Query Match 57.2%; Score 979; DB 24; Length 368;

Best Local Similarity 57.4%; Pred. No. 2e-79; Mismatches 88; Indels 2; Gaps 2;

Matches 189; Conservative 50; Mismatches 88; Indels 2; Gaps 2;

QY 2 EASGIGPE-VPDDRDFEPLSGVCPFCQCHLRVQCSDLGIDKVPKDLPPDTLLDION 60
DB 40 EASGADTSGVLDPSVPTTYSAMCFGCHLRVQCSDLGIDKSVPKETSPDTLLDION 99
QY 61 NKITEIKDGFKNLKNLHALILVNNKISKVSPGAFPTLVKLERLYLSKNOLKEPEKMPK 120
DB 100 NDISELRKDDFKGLDHLVYLVNNKISKIHEKAFSPRKQKLYISNHLVEIPNLP 159
QY 121 TLQELRAHENETTKYRKATFNGLNQMIYELGTNP LKSSGIENGAFQGMKKLSYRIADT 180
DB 160 SLVELRIHDNRIRKPKGVFSGLRNMNCIEMGNPLENSGEPGAFDGL-KLNYLRISBA 218
QY 181 NITSIPQGLPSPLETHLDGKISKVDAASLKGILNNLAKLGISFNSISAVDNGSLANTPH 240
DB 219 KLGTGPKDLPETLNEHLHDHKKIQAIIEEDLIRYSKLYRLGIGHNQIRMIENGSLFPT 278
QY 241 LRELHDNNKLTTRVPGGLAEHKYIQVYLVNNNISVVGSSDPFCPGHNTKASYSGVSLF 300
DB 279 LRELHDNNKLARVPSGLPDLKLQVYLVHSNNITKGVNDFCPMGFVGKAYNGISLF 338
QY 301 SNPQVWEIOPSTRCYVVRSAIQLGANYK 329
DB 339 NNVPVWEVQPATFRCTDRLAIOFGANYK 367

RESULT 17

AAE34394

ID AAE34394 standard; Protein; 368 AA.

XX AAE34394;

XX 14-MAY-2003 (first entry)

XX Human biglycan protein.

XX human; diagnosis; osteoarthritis; rheumatoid arthritis; biglycan.

XX Homo sapiens.

XX WO200295415-A2.

XX 28-NOV-2002.

XX 22-MAY-2002; 2002WO-EP05612.

XX 23-MAY-2001; 2001GB-0012626.

XX (OSTE-) OSTEOMETER BIO TECH AS.

XX Christgau S, Henriksen DB, Cloos PAC;

XX WPI; 2003-140389/13.

XX An assay for the diagnosis or assessment of the severity of an
PT osteoarthritis or rheumatoid arthritis comprising detecting an
PT isomerized or optically inverted protein in a sample -
PS Disclosure; Page 71-72; 106pp; English.

CC The invention relates to an assay for the diagnosis or assessment of
CC the severity of osteoarthritis or rheumatoid arthritis. The assay
CC involves measuring (in a biological sample) the amount or presence of
CC an isomerized or optically inverted protein or one or more isomerized
CC or optically inverted fragments from proteins such as perlecan,
CC biglycan, decorin, fibrillin-1 or procadherin. The assay is useful
CC for the diagnosis or assessment of the severity of osteoarthritis or
CC rheumatoid arthritis. The present sequence is human biglycan protein.

SQ Sequence 368 AA;

Query Match 57.2%; Score 979; DB 24; Length 368;

Best Local Similarity 57.4%; Pred. No. 2e-79; Mismatches 88; Indels 2; Gaps 2;

Matches 189; Conservative 50; Mismatches 88; Indels 2; Gaps 2;

QY 2 EASGIGPE-VPDDRDFEPLSGVCPFCQCHLRVQCSDLGIDKVPKDLPPDTLLDION 60
DB 40 EASGADTSGVLDPSVPTTYSAMCFGCHLRVQCSDLGIDKSVPKETSPDTLLDION 99
QY 61 NKITEIKDGFKNLKNLHALILVNNKISKVSPGAFPTLVKLERLYLSKNOLKEPEKMPK 120
DB 100 NDISELRKDDFKGLDHLVYLVNNKISKIHEKAFSPRKQKLYISNHLVEIPNLP 159
QY 121 TLQELRAHENETTKYRKATFNGLNQMIYELGTNP LKSSGIENGAFQGMKKLSYRIADT 180
DB 160 SLVELRIHDNRIRKPKGVFSGLRNMNCIEMGNPLENSGEPGAFDGL-KLNYLRISBA 218
QY 181 NITSIPQGLPSPLETHLDGKISKVDAASLKGILNNLAKLGISFNSISAVDNGSLANTPH 240
DB 219 KLGTGPKDLPETLNEHLHDHKKIQAIIEEDLIRYSKLYRLGIGHNQIRMIENGSLFPT 278
QY 241 LRELHDNNKLTTRVPGGLAEHKYIQVYLVNNNISVVGSSDPFCPGHNTKASYSGVSLF 300
DB 279 LRELHDNNKLARVPSGLPDLKLQVYLVHSNNITKGVNDFCPMGFVGKAYNGISLF 338
QY 301 SNPQVWEIOPSTRCYVVRSAIQLGANYK 329
DB 339 NNVPVWEVQPATFRCTDRLAIOFGANYK 367

RESULT 18

AAR87952

ID AAR87952 standard; Protein; 369 AA.

XX AAR87952;

XX 20-MAR-1996 (first entry)

XX Human neurotrophic biglycan.

XX Biglycan; proteoglycan; chondroitin sulphate; neuron protection;

XX neurotrophic; central nervous system; CNS; memory loss; dementia;

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..37

XX Region 44..60

XX W09530432-A1.

XX 16-NOV-1995.

PF 09-MAY-1994; 94WO-EP01479.
 XX
 PR 09-MAY-1994; 94WO-EP01479.
 XX
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 XX
 PI Hasenöehl R, Huston J, Junghans U, Kappler J, Koops A;
 PI Mueller HW;
 XX WPI; 1995-403938/51.
 DR
 XX
 PT Proteoglycan cpts., partic. chondroitin sulphate proteoglycan(s)
 PT for maintain structural and function of the CNS and attenuating
 PT memory deficit(s) in the elderly and patients with dementia
 XX
 PS Claim 3; Fig 8; 60pp; English.
 XX
 CC Human biglycan (AAR87952) is a chondroitin sulphate proteoglycan with
 CC neurotrophic activity for brain neurons. It can be used to enhance
 CC the survival and maintain the structure and function of CNS neurons
 CC during normal ageing as well as after pathological and/or traumatic
 CC nervous system damage. It can also be used to restore function
 CC following nervous system lesions and degenerative diseases, and to
 CC improve learning efficiency and memory in the elderly and in patients
 CC with dementia.
 CC
 SQ Sequence 369 AA;
 Query Match 57.1%; Score 978.5; DB 16; Length 369;
 Best Local Similarity 57.3%; Pred. No. 2.2e-79;
 Matches 189; Conservative 51; Mismatches 87; Indels 3; Gaps 2;
 QY 2 EASGIGPE--VPDRDEPESLGPVCPFRCCQCHLRVVOCSDLGLKAVPKDLPPTTLIDLQ 59
 DB 40 EASGADTTSGVLDPSVTPYTSAMCPGCHCHLRVVOCSDLGLKAVPKRISPDITLLDLQ 99
 QY 60 NNKTEIKDGFKNLKNLHLLIVNNKISKVSPGAFPLVLEBLYSKNQLKEPEKMP 119
 DB 100 NNDISELRKDPFKGLQHLVAVLVNNKISKIHEKAFSLRKLQKLYISKNLVETPPVLP 159
 QY 120 KTIQELRAHENEITKVKRTFNGINOMIVIELGTNPLKSGIENGAFQGMKKLSYIRIAD 179
 DB 160 SSVLELRHIDNRIRKVPKGVSGLRNNNCEIMGNGPLENSGFEPGAFDGL-KLNYLRRISE 218
 QY 180 TNTISIPQGLPPSLTEHLDNKTSRVDASLKLNLAKLGLSFNSISAVDNGSLANTP 239
 DB 219 AKLTGIPKDLPELTNELHLDHNKIQATELEDLRLYSKLYRGLGHNQIRMIENSLFLP 278
 QY 240 HLRHLHDNNKLTVPVPGGLAEHKYIOVYLLNNNISVVGSSDFCPGHNTKKASYSGVSL 299
 DB 279 TLREHLHDNNKLSRVPAGLPDLKLLQVYVYLLHNNITTKVGVNDFCPMGFGRARAYNGISL 338
 QY 300 FSNPVOYWEIOPSTFRCVYVSATQLGNKY 329
 DB 339 FNNPVPYWEVQPATFRCTVDRALAIQFGNXY 368
 RESULT 19
 ID AAR87953 standard; Protein; 332 AA.
 AC AAR87953;
 DT 20-MAR-1996 (first entry)
 DE Bovine neurotrophic biglycan.
 XX
 XX Biglycan; proteoglycan; chondroitin sulphate; neuron protection;
 KW neurotrophic; central nervous system; CNS; memory loss; dementia;
 XX learning.
 OS Bos taurus.
 XX

EH Key Location/Qualifiers
 FT Region 7..23
 XX /label= Hypervariable_region
 XX
 XX WO9530432-A1.
 XX
 XX PD 16-NOV-1995.
 XX
 XX
 PF 09-MAY-1994; 94WO-EP01479.
 PR 09-MAY-1994; 94WO-EP01479.
 XX
 XX (BOEF) BOEHRINGER MANNHEIM GMBH.
 PA
 PI Hasenöehl R, Huston J, Junghans U, Kappler J, Koops A;
 PI Mueller HW;
 XX WPI; 1995-403938/51.
 DR
 XX
 XX
 PT Proteoglycan cpts., partic. chondroitin sulphate proteoglycan(s)
 PT for maintain structural and function of the CNS and attenuating
 PT memory deficit(s) in the elderly and patients with dementia
 XX
 PS Claim 3; Fig 8; 60pp; English.
 XX
 CC Bovine biglycan (AAR87953) is a chondroitin sulphate proteoglycan with
 CC neurotrophic activity for brain neurons. It can be used to enhance
 CC the survival and maintain the structure and function of CNS neurons
 CC during normal ageing as well as after pathological and/or traumatic
 CC nervous system damage. It can also be used to restore function
 CC following nervous system lesions and degenerative diseases, and to
 CC improve learning efficiency and memory in the elderly and in patients
 CC with dementia.
 CC
 SQ Sequence 332 AA;
 Query Match 57.0%; Score 976.5; DB 16; Length 332;
 Best Local Similarity 57.1%; Pred. No. 2.9e-79;
 Matches 188; Conservative 51; Mismatches 87; Indels 3; Gaps 2;
 QY 2 EASGIGPE--VPDRDEPESLGPVCPFRCCQCHLRVVOCSDLGLKAVPKDLPPTTLIDLQ 59
 DB 3 EASGAEITSGIPDLDSLPPYTSAMCPGCHCHLRVVOCSDLGLKAVPKRISPDITLLDLQ 62
 QY 60 NNKTEIKDGFKNLKNLHLLIVNNKISKVSPGAFPLVLEBLYSKNQLKEPEKMP 119
 DB 63 NNDISELRKDPFKGLQHLVAVLVNNKISKIHEKAFSLRKLQKLYISKNLVETPPVLP 122
 QY 120 KTIQELRAHENEITKVKRTFNGINOMIVIELGTNPLKSGIENGAFQGMKKLSYIRIAD 179
 DB 123 SSVLELRHIDNRIRKVPKGVSGLRNNNCEIMGNGPLENSGFEPGAFDGL-KLNYLRRISE 181
 QY 180 TNTISIPQGLPPSLTEHLDNKTSRVDASLKLNLAKLGLSFNSISAVDNGSLANTP 239
 DB 182 AKLTGIPKDLPELTNELHLDHNKIQATELEDLRLYSKLYRGLGHNQIRMIENSLFLP 241
 QY 240 HLRHLHDNNKLTVPVPGGLAEHKYIOVYLLNNNISVVGSSDFCPGHNTKKASYSGVSL 299
 DB 242 TLREHLHDNNKLSRVPAGLPDLKLLQVYVYLLHNNITTKVGVNDFCPMGFGRARAYNGISL 301
 QY 300 FSNPVOYWEIOPSTFRCVYVSATQLGNKY 328
 DB 302 FNNPVPYWEVQPATFRCTVDRALAIQFGNXY 330
 RESULT 20
 ID AAG78510 standard; Protein; 368 AA.
 AC AAG78510;
 DT 29-JAN-2002 (first entry)
 XX

Db 40 EASGADTSGLDPSVTPTYSAMCPFGCHLRVVOCSDLGKSVPEISPDITLLDLQN 99
 QY 61 NKITEIKDGFKNLKNLHALILVNNKISKVSPGAFPLVLERLYLSKNQKELPERKPK 120
 Db 100 NDISLAKDPFKGQHLVYALVYNNKISKIHEKAFSPLRNQLKYLISKNHVEIPMLPS 159
 QY 121 TLOELRAHENEITYRKRTFNGLNQMTVIELGTNPLKSSGGENGAFOGKKLSTIRADT 180
 Db 160 SLVAVRIRHDIRKRVKGVSPFGLRNMCIEWGNPLENSGFEPGAFGL-CLNLTARISA 218
 QY 181 NITSIPQGLPSPLELHLDGKISRVDASLKGNNLAKLGLSPNSISAVDNGSLAMTPH 240
 Db 219 KLTGIPDLPETLWELHLDHKKIQALIEDDLRYSKYLRLGELHNOIMENSGLSLPLT 278
 QY 241 LREIHLNNKLTFRVPGGLAEHKYIQVYLNHNNISVVGSSDFCPGHNTKASYSVSLF 300
 Db 279 LREIHLNNKLTARVPSGLPDLKLIQVYLNHNNITKGVNDPCMGEGVKKAYNYSLE 338
 QY 301 SNPVQWEIQPSTFRVCYVRSALQGNK 329
 Db 339 NNVPVWEVGPATFRCTVDRILQFGNYK 367

RESULT 22

AAR42264
 ID AAR42264 standard; Protein; 186 AA.

XX AAR42264;

XX 25-MAR-2003 (updated)

DT 09-JAN-2003 (updated)

DT 28-APR-1994 (first entry)

XX Decorin sequence PT-75 (N-terminal to LRR6).

XX leucine-rich repeat; proteoglycan; cell regulatory factor; MBP;
 KM fusion protein; maltose binding protein; tumour growth; inhibition;
 KM decorin; PG-II; PG-40; transforming growth factor-beta; TGF-beta.

OS Bos sp.

PN WO9320202-A1.

PD 14-OCT-1993.

PF 02-APR-1993; 93WO-US03171.

PR 03-APR-1992; 92US-0865652.

XX (LJOL-) LA JOLLA CANCER RES FOUND.

PI Cardenas J, Craig W, Mullen DG, Pierschbacher MD;

PI Ruoslahti E;

DR WPI; 1993-336910/42.

DR N-PSDB; AA050050.

PT Active fragments of protein esp. decorin - with cell regulatory

PT factor domain, useful for inhibiting cell regulatory factor

XX Claim 10; Page 43-44; 77p; English.

CC Active fragments of decorin (full-length coding sequence AA050046)

CC were generated by PCR and fused to Maltose Binding Protein. The

CC resulting fusion proteins were useful for inhibiting the activity of

CC a cell regulatory factor, esp. TGF-beta, and hence for treating

CC conditions associated with over-activity of the growth factor such

CC as certain tumours.

CC (Updated on 09-JAN-2003 to add missing OS field.)

CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 186 AA;

XX SQ

Query Match 55.3%; Score 948; DB 14; Length 186;
 Best Local Similarity 100.0%; Pred. No. 4, 5e-77;
 Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 EASGIGPEVDDPSPSLQPVCPFRQCHLRVVOCSDLGKVPKDLPEDTLLDLQN 61
 Db 4 EASGIGPEVDDPSPSLQPVCPFRQCHLRVVOCSDLGKVPKDLPEDTLLDLQN 63
 QY 62 KITEIKDGFKNLKNLHALILVNNKISKVSPGAFPLVLERLYLSKNQKELPERKPK 121
 Db 64 KITEIKDGFKNLKNLHALILVNNKISKVSPGAFPLVLERLYLSKNQKELPERKPK 123
 QY 122 TLOELRAHENEITYRKRTFNGLNQMTVIELGTNPLKSSGGENGAFOGKKLSTIRADT 181
 Db 124 TLOELRAHENEITYRKRTFNGLNQMTVIELGTNPLKSSGGENGAFOGKKLSTIRADT 183
 QY 182 ITS 184
 Db 184 ITS 186

RESULT 23

AAB01311
 ID AAB01311 standard; Protein; 379 AA.

XX AAB01311;

XX 25-SEP-2000 (first entry)

XX Human PRO241 polypeptide.

XX PRO; membrane bound protein; secreted protein; PRO357; PRO327;

XX PRO243; PRO715; PRO241; PRO323; PRO299; PRO333; PRO344; PRO347;

XX PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide;

XX antibody; screening; detection; inhibition; probe; primer; human.

OS Homo sapiens.

XX Key

XX Location/Qualifiers

XX 1..15

XX /label= Signal peptide

XX /note= "N-myristoylation site"

XX Domain

XX /label= Leucine zipper pattern

XX /note= "N-myristoylation site"

XX Modified-site

XX /note= "N-myristoylation site"

XX Modified-site

XX /note= "N-myristoylation site"

XX Modified-site

XX /note= "N-glycosylation site"

XX Modified-site

XX /note= "N-myristoylation site"

XX WO200032776-A2.

XX 08-JUN-2000.

XX 01-DEC-1999; 99WO-US26301.

XX 01-DEC-1998; 98WO-US25108.

XX 16-DEC-1998; 98US-0112850.

XX 22-DEC-1998; 98US-0113296.

XX (GETH) GENENTECH INC.

PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E,
 PI Gerlitsen ME, Goddard A, Godowski PJ, Grimaldi CU, Gurney AL,
 PI Hillan KJ, Kijavini IU, Napier MA, Roy MA, Tamas D, Wood WI;
 DR WPI; 2000-412324/35.
 DR N-PSDB; AAA49551.
 XX
 PT New human nucleic acids encoding secreted and transmembrane
 PT polypeptides, designated as PRO polypeptides, useful as pharmaceutical
 PT and diagnostic agents
 PS
 PS Claim 12; Fig 2; 187pp; English.
 CC
 CC New human nucleic acids encoding secreted and transmembrane
 CC polypeptides which are designated as PRO polypeptides are described
 CC The membrane-bound proteins have various industrial applications,
 CC including as pharmaceutical and diagnostic agents. The membrane-bound
 CC proteins can also be employed for screening of potential peptide or
 CC small molecule inhibitors of the relevant receptor/ligand interaction.
 CC Anti-PRO antibodies are useful for the affinity purification of PRO
 CC from recombinant cell culture or natural sources.
 CC
 SQ Sequence 379 AA;
 Query Match 55.1%; Score 943.5; DB 21; Length 379;
 Best Local Similarity 55.0%; Pred. No. 3.2e-76;
 Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;
 Oy 11 PDDRPFEPFSLGVPFCPCCHLRVQCSDLGDKVPCDLPPTTLTLDLQNNKITEKDD 70
 Db 61 PSHFFPPFLFPMCPFGCCGCSRVVHCSDLGLTSVTNLPFDRLMDLQNNKITEKDD 120
 Oy 71 FNLNLNLHLLVNNKISVSPGAFPLVYKRLYLKSNQLKELPERMKTLOELRAHEN 130
 Db 121 FGLTSLVGLIINNNTLTIHPKAFITTKRLRLVLSHQLESLPLNLKSLAEIRHEN 180
 Oy 131 EITKTKRTKFNGLNQIVIELGNPLKSGIENGAGAQCKKLSYRIADNTITSIPGCLP 190
 Db 181 KVKKKIQKDTFKGMNMLHLEMSANPLDNNGISPGAEVGV-TVFHRIAEAKLTSPKGLP 239
 Oy 191 PELTEHLHDGKNSIRVDASLKGNNLNLATLGLSFNSISAVDNGSLANTPLRLHLDNNK 250
 Db 240 PTLLEHLHDYNKISTYLEDFPKRYKLOKLGANNKITIENSGLNITRVEHLNNK 299
 Oy 251 LTRVPGGLAEHKYIQVYVLLHNNNISVVGSSDFCPGHNTKKASYSVGSLSFNPVQYMEIO 310
 Db 300 LKKIPSGLELKLQITIFLHNSIARVGVNDFCTPTPKKKGLYSALSLFNNPVKYMEO 359
 Oy 311 PSTFRGVYRSALQGLNY 328
 Db 360 PATFRCVLSRMSVQLGNF 377
 RESULT 24
 AAU12335
 ID AAU12335 standard; Protein; 379 AA.
 AC AAU12335;
 DT 24-OCT-2001 (first entry)
 XX Human PRO241 polypeptide sequence.
 DE Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX WO200140466-A2.
 PN
 PD 07-JUN-2001.

XX
 PF 01-DEC-2000; 2000WO-US32678.
 XX
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 09-DEC-1999; 99US-0170262.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31243.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 24-FEB-2000; 2000WO-US05601.
 PR 01-MAR-2000; 2000WO-US07377.
 PR 20-MAR-2000; 2000WO-US07532.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 10-NOV-2000; 2000WO-US30873.
 XX
 PA (GENTH) GENENTECH INC.
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tamas D, Watanabe CK, Wood WI, Zhang Z;
 DR WPI; 2001-408281/43.
 DR N-PSDB; AAS21407.
 XX
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical
 PS
 PS Claim 12; Fig 328; 813pp; English.
 XX
 XX AAU12172-AAU12446 represent novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 CC
 SQ Sequence 379 AA;
 Query Match 55.1%; Score 943.5; DB 22; Length 379;
 Best Local Similarity 55.0%; Pred. No. 3.2e-76;
 Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

```

QY 11 PDDRDPEPSLGPVCPFCQCHLRVVOCSDLGLDKVPKDLPPDTLLDLONNKITEIKDGD 70
DB 61 PRSHFFPFDLPFPCPFQCCYSRVVHCSDDLGLTSVPTNIPDTMLDLONNKIKEIKEND 120
QY 71 FKNLKNLHALILVNKKISKVSPGAFPLVKLERLYLSKNQKEDPEKMPKTLQELRAHEN 130
DB 121 FKGLTSLYGLILNNKTLKIHKPAFLTTKKLRLLYSHNQSEIPLNPKSLAEIRHEN 180
QY 131 EITVRKVTENGILNQMIYIELGTNPLKSSGIENGAFQGMKKLSYIRIADTNTITSIPQGLP 190
DB 181 KVKKIQKOTFKGMALHVLHMSANPLDNNGIEPGAEGV-TVPHIRIAEAKLTSPKGLP 239
QY 191 PSTLHLDGKTKISRVDAASLGLNLLAKLGLSFNSISAVDNGSLANTPHLRHLDDNNK 250
DB 240 PTLLEHLHDYKNTLVELEDFRKYKELQRLGLGNKKITDIENGSLANIPVRAEIHLENNK 299
QY 251 LTRVPGGLAEHKYQIVVYLLNNNISVVGSSDFPCPGHNTKASVGSVLSFNPVQYMEIQ 310
DB 300 LKKTIPSGPELKYLQITFIHNSISIRVGVNDFCPTVPKMKSLYSALISLFFNPVKYMEMQ 359
QY 311 PSTFRCVYVRSALQIGNTY 328
DB 360 PATFRCVLSRMSVQLGNF 377

RESULT 25
ABB95437
ID ABB95437 standard; Protein; 379 AA.
XX
AC ABB95437;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related protein PRO241 SEQ ID NO: 30.
XX
KM Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KM atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KM cardiac; cystostatic; antiangiogenic; hypotensive; vulnerary;
KM antiarteriosclerotic.
XX
OS Homo sapiens.
XX
PN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US21735.
XX
XX 20-JUL-2000; 2000US-219556P.
XX 25-JUL-2000; 2000US-220634P.
XX 25-JUL-2000; 2000US-220664P.
XX 28-JUL-2000; 2000WO-US20710.
XX 02-AUG-2000; 2000US-222695P.
XX 17-AUG-2000; 2000US-0643657.
XX 23-AUG-2000; 2000WO-US23522.
XX 24-AUG-2000; 2000WO-US23328.
XX 07-SEP-2000; 2000US-230978P.
XX 15-SEP-2000; 2000US-000000P.
XX 18-SEP-2000; 2000US-0664610.
XX 18-SEP-2000; 2000US-0665350.
XX 24-OCT-2000; 2000US-242922P.
XX 08-NOV-2000; 2000US-0709238.
XX 08-NOV-2000; 2000WO-US30952.
XX 10-NOV-2000; 2000WO-US30873.
XX 01-DEC-2000; 2000WO-US32678.
XX 20-DEC-2000; 2000US-0747259.
XX 20-DEC-2000; 2000WO-US34956.
XX 22-JAN-2001; 2001US-0767609.
XX 28-FEB-2001; 2001US-0796498.
XX 28-FEB-2001; 2001WO-US06520.
XX 01-MAR-2001; 2001WO-US06666.
XX 09-MAR-2001; 2001US-0802706.

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PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0864280.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 28-JUN-2001; 2001WO-US00000.
XX
PA (GERTH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERB) FERRARA N.
PA (GERB) GERBER H.
PA (GERB) GERRITSEN M E.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GURN) GURNEY A L.
PA (HILL) HILLAN K J.
PA (MARS) MARSTERS S A.
PA (PANJ) PAN J.
PA (PAON) PAONI N F.
PA (STEP) STEPHAN J F.
PA (WATA) WATANABE C K.
PA (WILL) WILLIAMS P M.
PA (WOOD) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF,
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W,
XX
DR WPI; 2002-171999/22.
DR N-PSDB; ABL95575.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
PS Claim 11; Fig 30; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention.
XX
SQ Sequence 379 AA;

```

Query Match 55.1%; Score 943.5; DB 23; Length 379;
Best Local Similarity 55.0%; Pred. No. 3.2e-76;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

```

QY 11 PDDRDPEPSLGPVCPFCQCHLRVVOCSDLGLDKVPKDLPPDTLLDLONNKITEIKDGD 70
DB 61 PRSHFFPFDLPFPCPFQCCYSRVVHCSDDLGLTSVPTNIPDTMLDLONNKIKEIKEND 120
QY 71 FKNLKNLHALILVNKKISKVSPGAFPLVKLERLYLSKNQKEDPEKMPKTLQELRAHEN 130
DB 121 FKGLTSLYGLILNNKTLKIHKPAFLTTKKLRLLYSHNQSEIPLNPKSLAEIRHEN 180
QY 131 EITVRKVTENGILNQMIYIELGTNPLKSSGIENGAFQGMKKLSYIRIADTNTITSIPQGLP 190
DB 181 KVKKIQKOTFKGMALHVLHMSANPLDNNGIEPGAEGV-TVPHIRIAEAKLTSPKGLP 239
QY 191 PSTLHLDGKTKISRVDAASLGLNLLAKLGLSFNSISAVDNGSLANTPHLRHLDDNNK 250

```

DB 240 PTLLEHLIDGNKSTVELEDFKRYKELQRLGLGNKTTIDLENSLANIPRAVEIHLENNK 299
QY 251 LTRVPGGLAEHKYIQVYVYLNHNNSIVVSGSDPCPGHNTKASYSVGSVLSFNPVQYWEIQ 310
DB 300 LKKIPFGLPELKYLIQIIFLHNSIARVGVNDFCPVPMKKSLYSALSIFNPNVKTWEMQ 359
QY 311 PSTFRVCVYRSALQLGNY 328
DB 360 PATFRCLSRMSVOLGNF 377

RESULT 26
ABU6733
ID ABB84831 standard; Protein; 379 AA.
AC ABB84831;
XX
XX 16-MAY-2002 (first entry)
DE Human PRO241 protein sequence SEQ ID NO:30.
XX
XX Human; angiogenesis; cardiac; cytosolic; antiangiogenic; hypotensive;
XX vulnerable; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
XX gene therapy; cardiovascular disorder; endothelial disorder; cancer;
XX angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
XX age-related macular degeneration; arterial restenosis; angina;
XX rheumatoid arthritis; myocardial infarction; thrombophlebitis;
XX lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
XX wound healing; chromosome mapping; gene mapping.
OS Homo sapiens.
XX
XX WO200200690-A2.
PN
XX 03-JAN-2002.
PD
XX 20-JUN-2001; 2001MO-US19692.
PF

XX (GETH) GENENTECH INC.
PA Baker KP, Ferrara N, Garber H, Gerritsen ME, Goddard A, Goddard A,
XX Goddard PJ, Gurney AL, Hillen KJ, Marsters SA, Pan J, Paoni NF,
PI Godwin JF, Watanabe CK, Williams FW, Wood WI, Ye W,
PI Stephan WJ, Watanabe CK, Williams FW, Wood WI, Ye W,
XX MPI; 2002-090516/12.
DR N-PSDB; ABL88086.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
XX Claim 11; Fig 30; 565bp; English.
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiac, cytosolic,
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
CC degeneration, atherosclerosis, hypertension, arterial restenosis,
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
CC carcinoma) and wound healing. The PRO polynucleotides have applications
CC in molecular biology, including use as hybridisation probes, and in
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC probes used in the exemplification of the present invention.
XX
XX Sequence 379 AA:
SQ

Query Match 55.1%; Score 943.5; DB 23; Length 379;
Best Local Similarity 55.0%; Pred. No. 3.2e-76;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;
QY 11 PDDRFEPISLIGVCPFCQCHLRVQCSDLGLKVPKDPPTTLTDLGNKITEIKDGP 70
DB 61 PRSHPPPLPFMCPFCGCGCYRVNHCSDGLTSVPTNIPPTRMDLGNKITEIKEND 120
QY 71 PKLKLHLLIYNKISVSPGAPFVYKLELYTSKQQLKELPKMFKYLOELRAHEN 130
DB 121 FKGLTSLYGLIINNNTLTIHPKAFITTKLRRLYSHNQLSEIPIPLPKSLAELEIRHN 180
QY 131 BITKRVKVTENGANGIVLELGTNPXSSGSGANGQMKKLSYRIADNTNITSIQGP 190
DB 181 KVKIKQKOTFKGNALHVEMSANPLDNNNGIEPGAFEGV-TVFHRIARAKLTSPKGLP 239
QY 191 PSTLEHLIDGNKISRVDASLKLNNIATLGLSPNSISAVDNGSLANTPHLEHLIDNNK 250
DB 240 PTLLEHLIDGNKSTVELEDFKRYKELQRLGLGNKTTIDLENSLANIPRAVEIHLENNK 299
QY 251 LTRVPGGLAEHKYIQVYVYLNHNNSIVVSGSDPCPGHNTKASYSVGSVLSFNPVQYWEIQ 310
DB 300 LKKIPFGLPELKYLIQIIFLHNSIARVGVNDFCPVPMKKSLYSALSIFNPNVKTWEMQ 359
QY 311 PSTFRVCVYRSALQLGNY 328
DB 360 PATFRCLSRMSVOLGNF 377

RESULT 27
ABU6733
ID ABU6733 standard; Protein; 379 AA.
AC ABU6733;
XX
XX 23-MAY-2003 (first entry)
DE Human PRO polypeptide #164.
XX
XX Human; PRO polypeptide; secreted and transmembrane protein;

KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
 KW differentiation; chondrocyte; tumour; genetic disorder;
 KW cytostatic.
 OS Homo sapiens.
 PN US2003036180-A1.
 XX
 XX 20-FEB-2003.
 PD
 PF 09-MAY-2002; 2002US-0143114.
 XX
 XX 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 16-SEP-1998; 98WO-US19177.
 PR 17-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 07-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22391.
 PR 29-OCT-1998; 98WO-US22392.
 PR 29-OCT-1998; 98WO-US24855.
 PR 29-OCT-1998; 98WO-US25108.
 PR 01-DEC-1998; 98WO-US25106.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US05028.
 PR 10-MAR-1999; 99WO-US05190.
 PR 20-APR-1999; 99WO-US08615.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30035.
 PR 20-DEC-1999; 99WO-US30911.
 PR 22-DEC-1999; 99WO-US30999.
 PR 22-DEC-1999; 99WO-US30720.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 10-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.

PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US34956.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 26-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0806889.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 16-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
 PI Gerltsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI; 2003-332040/31.
 DR N-PSDB; AOA03766.
 XX
 XX New secreted and transmembrane PRO nucleic acids, useful for gene
 PT therapy, in chromosome and gene mapping, as chromosome markers, in
 PT tissue typing, and in chromosome identification -
 XX
 XX
 PS Claim 12; Fig 328; 660pp; English.
 XX
 XX The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists.
 CC The PRO polypeptides are useful for stimulating the release of
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating the
 CC proliferation or differentiation of chondrocytes, and detecting the
 CC presence of tumours. The polynucleotide sequences encoding PRO
 CC polypeptides are useful as hybridisation probes, in chromosome and
 CC gene mapping, in the generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptides, for generating transgenic animals or
 CC knockout animals, for the genetic analysis of individuals with genetic
 CC disorders, and in gene therapy. AB06570-AB06684 represent the human
 CC PRO polypeptides of the invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at

CC segdata.uspto.gov/psipdedentry.html.
XX Sequence 379 AA;
SQ
Query Match 55.1%; Score 943.5; DB 24; Length 379;
Best Local Similarity 55.0%; Pred. No. 3.2e-76;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;
QY 11 PDDRFEPSLGAVCPFCQCHLRVVOCSDLGLKVPKIDLPPTTLIDLONNKITEKOD 70
DB 61 PRSHFFPFDLPFCPFPGCCGSRVHCSDLGLTSVPTNIPFTRLIDLONNKIKIKEND 120
QY 71 FKNLNLHLLILVNNKISKVSGALFPLVYKLERLISKQKELPEKPKYLOELPAHEN 130
DB 121 FGLTSLGLILNNKLTIKHPKAFYTKKLRLYLSHNQLSEIPLNLPKSLAEIRIHEN 180
QY 131 EITVKRVTFNGINQIVIEELGNPLKSSGIENGAFQGGKKLSYRIRIDNTNISTPQGLP 190
DB 181 KVKKIQKOTFKGMNMLHVEEMANPLDNGIEFGAFEGV-TVFHIRIAAKLTSPKGLP 239
QY 191 PELTEIHLIDGNKISRVDASLKLNNLAKLGLSFNSISAVDNGSLANTEPHLREHLIDNNK 250
DB 240 PTLTEIHLIDYNNKISTVELEDPRKRYKELQRLGLGNKKITDIENGSLANIPRAVEIHLENNK 299
QY 251 LTRVGGGLAEHKYIQVVIHANNISVSGSDPCPGHNTKAKSYSGVSLFSPVQYWEIQ 310
DB 300 LKRTSSGLPELKYLDIIFLHNSIARVGVNDPCPTVPKMKSLYSALISFNNPVKXWEMQ 359
QY 311 PSTFCVYVRSALQIGNY 328.
DB 360 PATFRCVLSRMSVQLGNP 377
RESULT 28
ABU67009
ID ABU67009 standard; Protein; 379 AA.
XX AC ABU67009;
XX DT 27-MAY-2003 (first entry)
XX DE Human secreted/transmembrane, PRO, protein SEQ ID 328.
XX KW Human; secreted protein; transmembrane protein; PRO;
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defects; premature aging; AIDS; biosensor;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW bioindicator; tumour.
XX OS Homo sapiens.
XX PN US2003032155-A1.
XX PD 13-FEB-2003.
XX PF 03-MAY-2002; 2002US-0137865.
XX 31-MAR-1997; 97WO-US05230.
XX 12-JUN-1998; 98WO-US12456.
XX 14-JUL-1998; 98WO-US14552.
XX 28-AUG-1998; 98WO-US17888.
XX 10-SEP-1998; 98WO-US18824.
XX 14-SEP-1998; 98WO-US19093.
XX 14-SEP-1998; 98WO-US19094.
XX 16-SEP-1998; 98WO-US19177.
XX 17-SEP-1998; 98WO-US19330.
XX 17-SEP-1998; 98WO-US19437.
XX 29-OCT-1998; 98WO-US21141.
XX 29-OCT-1998; 98WO-US22991.
XX 29-OCT-1998; 98WO-US22992.
XX 20-NOV-1998; 98WO-US24855.
XX 01-DEC-1998; 98WO-US25108.
XX 05-JAN-1999; 99WO-US00106.

PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 30-NOV-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 22-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 10-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06319.
PR 20-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US07532.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30973.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000WO-US27259.
PR 28-FEB-2001; 2001US-079648.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.

PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX
 PA (BETH) GENENTECH INC.
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI; 2003-331925/31.
 DR N-PSDB; ACA04187.
 XX
 PT New secreted and transmembrane nucleic acids and polypeptides,
 PT designated as PRO, useful for treating inflammation, organ failure,
 PT atherosclerosis, cardiac injury, infertility, birth defects, premature
 PT aging, AIDS, or cancer
 PT
 XX
 PS Claim 12; Fig 328; 659pp; English.
 CC The invention relates to an isolated nucleic acid comprising, or which is
 CC at least 80% identical to, or the full-length coding sequence of, any of
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid
 CC further comprises the full-length coding sequence of the DNA deposited
 CC under American Type Culture Collection (ATCC) accession number in a list
 CC given in the specification. Also included are vectors and host
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
 CC antibodies, PRO extracellular domains and mature sequences, methods
 CC of detecting PRO proteins, methods for stimulating the release of
 CC TNF-alpha (tumour necrosis factor alpha) from human blood,
 CC (and the proliferation of differentiation of chondrocyte cells, the
 CC proliferation of, or gene expression in pericyte cells, the release or
 CC proteoglycans from cartilage, proliferation of inner ear utricular
 CC supporting cells, the proliferation of T-lymphocyte cells, the release
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
 CC proliferation of endothelial cells), a method for modulating the uptake
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
 CC a method for inhibiting the binding of A-peptide to factor VIIa,
 CC or the differentiation of adipocyte cells, a method for detecting the
 CC presence of a tumour in a mammal and an oligonucleotide probe derived
 CC from any of the nucleotide sequences cited above. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
 CC diabetic complications. The nucleic acids are useful as hybridisation
 CC probes, in chromosome and gene mapping, and in generating antisense RNA
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
 CC biosensors or bioreactors. Both are useful in tissue typing.
 CC The present sequence represents a PRO protein of the invention.
 CC
 XX
 SQ Sequence 379 AA;
 Query Match 55.1%; Score 943.5; DB 24; Length 379;
 Best Local Similarity 55.0%; Pred. No. 3.2e-76;
 Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;
 QY 11 PDDRDEPSLGVPCPRCCCHLRVQCSLDLKVPKDLPPTTLADLNNKITEIKXGD 70
 DB 61 PRSHFPFPLPMPCCPGCCQCYSSVHAGCSLDGLTSVPTNIPDTRMDLNNKIKKIKEND 120
 QY 71 PKNLKLHLLILVNNKISKVSPAFPLVLTERTVLSKQKELPKMKPTQELFAHFN 130
 DB 121 FKGLTSLYGLILNNNNLTKIHPAFLTTKRLRLVYSHQSLSTIPNLPSIAELAIHFN 180
 QY 131 EITKVKATVFNGILNQMIIVIELGTNPSSGSIENGAFQGMKKLSYIRIADTNITSIPQGP 190

DB 181 KVKKIKQDIFPKGNALHVEMSANPLDNNGIEGAEVGV-TVPHIKAEKLTSPKGLP 229
 QY 191 PSTLEHLIDGNKISRVDASIKGLNMLAKGLSFPNSISAVDNGSLANTPHLREHLDDNNK 250
 DB 240 PTLLEHLIDNNKISTYBELDFPKYKXELQRLGLDNNKITDLENSLANNIPVREHLDDNNK 299
 QY 251 LTRVPGGLAEHKYIQVYVYLNNNISVVGSSDFPCPPGHNTYKASVGVLSFNPQVWEIQ 310
 DB 300 LKKIPSGLPFLKTLQITFLHSNLSIARVGVDFCPTVPKMKKSLYSALISLFPNPKWEMQ 359
 QY 311 PSTPRCYVNSAIOLENTY 328
 DB 360 PATFRCVLSRMSVQLGNF 377
 RESULT 29
 AB067121
 ID AB067121 standard; Protein; 379 AA.
 AC AB067121;
 XX
 AC 27-MAY-2003 (first entry)
 DT
 XX
 DE Human PRO polypeptide #1.
 XX
 KW Human; PRO; neurodegenerative disorder; Alzheimer's disease;
 KW Parkinson's disease; neural damage; trauma; inflammatory disease; AIDS;
 KW chemotherapy; organ failure; atherosclerosis; cardiac injury; diabetes;
 KW infertility; birth defect; premature aging; tumour; wound healing;
 KW cancer; neuroprotection; neuroprotective; anti-HIV; antidiabetic; cardiac;
 KW antiatherosclerotic; antiinflammatory; antiparkinsonian; cytostatic;
 KW antiinfectivity; vulnerary.
 KW
 XX
 OS Homo sapiens.
 XX
 FN US2002165143-A1.
 PD
 XX
 PD 07-NOV-2002.
 PF
 XX
 PF 30-AUG-2001; 2001US-0944403.
 PR 16-SEP-1998; 98WO-US19330.
 PR 01-DEC-1998; 98WO-US25108.
 PR 22-JUN-1999; 99WO-US12252.
 PR 15-SEP-1999; 99WO-US21090.
 PR 30-NOV-1999; 98WO-US28313.
 PR 30-NOV-1999; 98WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 16-DEC-1999; 99WO-US30095.
 PR 11-FEB-2000; 2000WO-US0365.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 03-DEC-1997; 97US-067411P.
 PR 11-DEC-1997; 97US-069278P.
 PR 11-DEC-1997; 97US-069334P.
 PR 11-DEC-1997; 97US-069335P.
 PR 12-DEC-1997; 97US-069425P.
 PR 16-DEC-1997; 97US-069694P.
 PR 16-DEC-1997; 97US-069696P.
 PR 16-DEC-1997; 97US-069702P.
 PR 17-DEC-1997; 97US-069870P.
 PR 17-DEC-1997; 97US-069873P.
 PR 18-DEC-1997; 97US-068017P.
 PR 05-JAN-1998; 98US-070440P.
 PR 09-FEB-1998; 98US-074086P.
 PR 09-FEB-1998; 98US-074092P.
 PR 25-FEB-1998; 98US-075945P.

PR 16-DEC-1998; 98US-112850P.
 PR 22-DEC-1998; 98US-113296P.
 PR 28-JUL-1999; 99US-146222P.
 PR 25-MAY-2001; 2001US-0866028.

XX (GETH) GENENTECH INC.

PI Baker KP, Borstein D, Baton DL, Ferrara N, Filvaroff E,
 PI Geritseen ME, Goddard A, Godowski PJ, Grimaldi JC, Gunney AL,
 PI Hillan KJ, Kijavrin JU, Napier WA, Roy MA, Tumas D, Wood WI,

DR WPI; 2003-288142/28.
 DR N-PSDB; ACA04301.

PT New PRO polypeptides and nucleic acid molecules, useful in diagnosing
 PT or treating inflammatory diseases, organ failure, atherosclerosis,
 PT cardiac injury, infertility, cancer, AIDS, Alzheimer's disease or
 PT Parkinson's disease -

PS Claim 12; Fig 2; 17pp; English.

XX The invention relates to an isolated human PRO polypeptide and the
 CC polynucleotide encoding it. The PRO polypeptides and nucleic acids are
 CC useful in diagnosing or treating neurodegenerative disorders such as
 CC Alzheimer's disease or Parkinson's disease, and neural damage, e.g. due
 CC to trauma or after chemotherapy, inflammatory disease, organ failure,
 CC atherosclerosis, cardiac injury, infertility, birth defects, premature
 CC aging, AIDS, diabetic complications and mutations in general. The
 CC polypeptides are useful for diagnosing tumours, or for inhibiting the
 CC growth of tumour cells. The polypeptides are also useful for wound
 CC healing and associated therapies concerned with re-growth of tissue. The
 CC polynucleotide sequences may be used as hybridisation probes in
 CC chromosome and gene mapping, or in generating antisense RNA and DNA. PRO
 CC nucleic acids are also useful in preparing PRO polypeptides, in assays to
 CC identify other proteins or molecules involved in binding reactions, and
 CC to generate transgenic or knockout animals, which in turn are useful in
 CC the development and screening of therapeutically useful reagents for
 CC chromosome identification and tissue typing. The PRO sequences are also
 CC useful in gene therapy and as molecular weight markers for protein
 CC electrophoresis purposes. Sequences ABU67121-ABU67136 represent human PRO
 CC polypeptides of the invention.

XX Sequence 379 AA;

Query Match 55.1%; Score 943.5; DB 24; Length 379;

Best Local Similarity 55.0%; Pred. No. 3.2e-76;

Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDRDEPSLGPVCPRCOCHLRVOCSDLGDKVXKDLPRPTTLLDQNNKITEKGD 70
 Db 61 PSHHPFPDLPFCPCGCGCYSIVHCSGLSVPTNIPPTRMLDQNNKIKETKEND 120
 QY 71 FKNLKLHALLIVNNKISKVSFGAFTPLVKEELYSKQNLKELPEKMPKTYOELRAHEN 130
 Db 121 FKGLTSLYGLILNNNKLTKIHPKAFLTTKKRLRLYSHQOLBEIPNLPSLAEARIHEN 180
 QY 131 ELTKRKATFENGLOMIVIELGNPLKSSGIENGAFQCKKLSYRIADNTITSIPQGLP 190
 Db 181 KVKKKQKQDFKGMNNAHVLMEGSAANPLDNNGIEGAFEGV-TVFHRIAEAKLTSVPKGP 239
 QY 191 PSLTEHLHDGKNTSRVDAASLKLGNLNLALGLSPNSISAVDNGSLANTPHLEIHLDNKK 250
 Db 240 PTLBSHLHDYNNKISTYELDFPKRYKELQRLGANNKTIIDENGSLANITRVEIHLNKK 299
 QY 251 LTRVPGGLAEKRYIQVYLLHNNNISVVGSDPCPGPHNTKKSYSVSLFSNPVQWETO 310
 Db 300 LKKIRSGLPBELKYLQIIFLHNSIARVGVNDFCPTVPKMKSLYSALISLFPNPKWEMQ 359
 QY 311 PSTERCYVRSALQAGNY 328
 Db 360 PATFRCVLSRMSVQAGNF 377

RESULT 30
 ABUS9814
 ID ABUS9814 standard; Protein; 379 AA.
 XX
 AC ABUS9814;
 XX
 DT 13-MAY-2003 (first entry)
 XX
 DE Novel secreted and transmembrane protein PRO241.
 XX
 KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
 KW cardiac insufficiency disorder; cancer; tumour; immune response;
 KW adrenal cortical capillary endothelial growth; c-fos induction;
 KW vascular endothelial growth factor inhibition; VEGF inhibition;
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
 KW retinal neurons cell survival; rod photoreceptor cell survival;
 KW retinal disorder; retinitis pigmentosa; kidney disorder;
 KW mammalian kidney mesangial cell proliferation; Berger disease;
 KW dermatitis; herpeticiformis; Cronn's disease; chondrocyte proliferation;
 KW chondrocyte redifferentiation; sports injury; arthritis.
 XX
 OS Homo sapiens.
 XX
 PN US2003017563-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 07-MAY-2002; 2002US-0140808.
 XX
 PR 31-MAR-1997; 97WO-US06230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 07-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22991.
 PR 29-OCT-1998; 98WO-US22992.
 PR 20-NOV-1998; 98WO-US24855.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US05026.
 PR 10-MAR-1999; 99WO-US05190.
 PR 20-APR-1999; 99WO-US08615.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 22-DEC-1999; 99WO-US30720.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.

XX PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0806889.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.

XX PA (GETH) GENENTECH INC.
XX
PI Baker KP, Benesini M, DeForge L, Desnoyers L, Filyaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S,
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;
XX
DR MPI, 2003-148238/14.
DR N-PSDB; ABX89304.

XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT are therapeutically useful for enhancing proliferation of stimulated T-lymphocytes
PT treatments -
XX
PS Claim 12; Fig 328; 659pp; English.
XX

The invention describes an isolated human PRO polypeptide. The PRO

polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186 stimulate adrenal cortical capillary endothelial growth, and PRO536, PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126, PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antenatal of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of retinal neurons cells (PRO1132 is also enhances survival/proliferation of rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813 and PRO1106 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpeticiforms or Crohn's disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein.

Query Match 55.1%; Score 943.5; DB 24; Length 379;
 Best Local Similarity 55.0%; Pred. No. 3.2e-76;
 Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

Qy	11	PDDDDFEESLEPVCPEFRQOCHLRVQOCSIDLGLDJKVPKLPBPTTLLDLONNKI TEIKOD	70
Db	61	PRSHFPFDPLEPMWCFQGCYSRVVHGSDLGLTSPTMNI PFDTMRMDLONNKI KEIKEND	120
Qy	71	FKNLKNHALLLVNNKISKVSPGATPLVLEKRLVLSKOKLEPEKMKTOELPAHFN	130
Db	121	FKGLTSLGLLLNNKKTTPKHPKAVLTTKCARLTLSHQSELPINLEPKSLAEHLIHN	180
Qy	131	EITFKRVKTFENGLNOMIVIELGTNPLESKSGIENGAFQOGKKLSYIRIADNTITSIPQLE	190
Db	181	KVKKIIOKOTFGGMANAHVLEMSANPLDNNNGIEPGAEGV-TVFHIRIAEAKTSVPEKLE	239
Qy	191	PSLTELHLDGKKISKISRVDAASLKGLLNNLAKLGLSFNLSIAVDNGISANTHEHLEHLDNK	250
Db	240	PTLLEHLDHYKISITVELDEDFRKYELQRLGLGNKKRTYDIENGSLANIRVBEHLENNK	299
Qy	251	LTRVPGGLAEHKYIQVIVLANNNTISVWSSDPCCPGHNHTKKASVGSVLSFNPVOYWEIO	310
Db	300	LKKIPSGELPELKTQIILFIHSNISIRVGVNDCECPVPMKKKSLYSAISLEFNNPVKYMEO	359
Qy	311	PESTRCVYVBSAIDQNGY 328	
Db	360	PATFRCVLSRMSVOLDGNF 377	

Search completed: February 9, 2004, 11:35:56
Job time : 81 secs

The invention describes an isolated human PRO polypeptide. The PRO

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2004, 11:21:34 ; Search time 38 seconds

(without alignments)
832.618 Million cell updates/sec

Title: US-10-004-176-6

Perfect score: 1713
Sequence: 1 VEASGLGPEVDDRDPEPSL.....QPSTRCVYVSATQLGNVYK 329

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 76:*

1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1709	99.8	359	1	NEHUC8
2	1564.5	91.3	360	2	S06280
3	1564.5	91.3	360	2	S06280
4	1415	82.6	357	2	S24317
5	1365.5	79.7	354	2	A55454
6	1331.5	77.7	354	2	S29145
7	985.5	57.5	369	2	S32793
8	984.5	57.5	369	2	S20811
9	982.5	57.4	369	2	S32559
10	979	57.2	368	1	BGHUN
11	385.5	22.5	382	2	I39068
12	365.5	21.3	343	2	A41748
13	365.5	20.8	342	2	A46743
14	347.5	20.1	338	2	S52284
15	327.5	19.1	1523	2	T13953
16	327	19.1	1523	2	T13953
17	326.5	19.1	376	2	S55275
18	323	18.9	1469	2	B36665
19	323	18.9	1480	2	A36665
20	314.5	18.4	375	2	S05390
21	314	18.3	1025	2	T42626
22	298.5	17.4	380	2	S71876
23	295.5	17.3	307	2	J60176
24	293	17.1	361	2	A53860
25	291	17.0	1091	2	A58532
26	285.5	16.7	907	2	UC0193
27	283.5	16.5	707	2	UC7163
28	273	15.9	605	2	JC5239
29	273	15.9	605	2	A41915

30	272	15.9	603	2	JC1282	insulin-like growth
31	264.5	15.4	603	2	JC6128	insulin-like growth
32	261	15.2	680	2	T19939	hypothetical prote
33	254	14.8	316	2	A41781	proteoglycan-1b -
34	252.5	14.7	322	2	S72271	proteoglycan-1b pr
35	248.5	14.5	536	2	A34901	lysine carboxypept
36	246.5	14.4	1389	2	T13852	gene wheeler prote
37	244	14.2	738	2	T13938	hypothetical prote
38	240.5	14.0	1385	2	T13887	tilr protein - frui
39	238	13.9	298	2	UC4130	osteoglycin precu
40	236.5	13.8	560	2	A60164	platelet membrane
41	233	13.6	594	2	T23841	hypothetical prote
42	231.5	13.5	333	2	T34555	hypothetical prote
43	231.5	13.5	662	2	S42799	garp precursor - h
44	231	13.5	610	2	T23836	hypothetical prote
45	226	13.2	2493	2	A55481	adenylate cyclase

ALIGNMENTS

RESULT 1
NEHUC8
decorin precursor - human
N/Alternate names: cartilage proteoglycan protein II; DS-Pg II; PG40 core protein; pr
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1988 #sequence revision 30-Jun-1988 #text_change 21-Jan-2000
C/Accession: A45016; A45015; B45015; A26476; S06640
R/Vetter, U.; Vogel, W.; Jue, W.; Young, M.F.; Fisher, L.W.
Genomics 15, 161-168, 1993
A/Title: Human decorin gene: intron-exon organization, discovery of two alternati
A/Reference number: A45016; MUID:93162643; PMID:8432527
A/Accession: A45016
A/Molecule type: DNA
A/Residues: 1-359 <VER>
A/Cross-references: GB:L01125; GB:L01126; GB:L01127; GB:L01128; GB:L01129; GB:L01130;
A/Note: sequence extracted from NCBI backbone (NCBIP:125061)
R/Danielson, K.G.; Fazzio, A.; Cohen, I.; Cannizzaro, L.A.; Bichteler, I.; Iozzo, R
Genomics 15, 146-160, 1993
A/Title: The human decorin gene: intron-exon organization, discovery of two alternati
A/Reference number: A45015; MUID:93162642; PMID:8432526
A/Accession: A45015
A/Status: not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 28-70 <DA2>
A/Cross-references: GB:M98262
A/Note: sequence extracted from NCBI backbone (NCBIP:125013)
A/Accession: B45015
A/Status: not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 236-359 <DAN>
A/Note: sequence extracted from NCBI backbone (NCBIP:125017)
R/Krusius, T.; Ruoslahti, E.
Proc. Natl. Acad. Sci. U.S.A. 83, 7683-7687, 1986
A/Title: Primary structure of an extracellular matrix proteoglycan core protein deduc
A/Reference number: A26476; MUID:87017013; PMID:3484330
A/Accession: A26476
A/Molecule type: mRNA
A/Residues: 1-359 <KRU>
A/Cross-references: GB:M14219; NID:G181169; PIDN:AA800774.1; PID:G181170
R/Roughley, P.J.; White, R.J.
Biochem. J. 262, 823-827, 1989
A/Title: Dermatan sulphate proteoglycans of human articular cartilage. The properties
A/Reference number: S05639; MUID:90073579; PMID:2590169
A/Accession: S05640
A/Molecule type: protein
A/Residues: 31-33, 'X', 35-50 <ROU>
C/Comment: This protein binds type I collagen.
C/Genetics:
A/Gene: GDB:DCN
A/Cross-references: GDB:119839; OMIM:125255
A/Map position: 12q21.3-12q23
A/Introns: 71/1; 108/3; 180/1; 218/1; 249/2; 295/3

A>Note: the first two introns occur before the initiator codon
 C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan
 C:Keywords: Chondroitin sulfate proteoglycan; collagen binding; dermatan sulfate; dupli
 F:1-16/Domains: signal sequence #status predicted <PRO>
 F:17-30/Domains: proteoglycan #status predicted <PRO>
 F:31-359/Product: decorin #status predicted <PRO>
 F:48-72/Domains: proteoglycan amino-terminal homology <PAH>
 F:82-105/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F:106-129/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:130-150/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F:151-174/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
 F:175-200/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
 F:201-221/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
 F:222-245/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
 F:246-269/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
 F:270-292/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
 F:293-316/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
 F:308-359/Domains: proteoglycan carboxyl-terminal homology <PC>
 F:34/Binding site: dermatan sulfate (Ser) (covalent) #status experimental
 F:189,325/Binding site: dermatan sulfate (Ser) (covalent) #status predicted
 F:211,262,303/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.8%; Score 1709; DB 1; Length 359;
 Best Local Similarity 100.0%; Pred No. 9, 5e-116; Indels 0; Gaps 0;
 Matches 328; Conservative 0; Mismatches 0;
 QY 2 EASGIGPEVDDHDFPSPGAPVPCFPCQCHLRVQCSDDLGLKVPDLPPDTLLDLDQNN 61
 DB 32 EASGIGPEVDDHDFPSPGAPVPCFPCQCHLRVQCSDDLGLKVPDLPPDTLLDLDQNN 91
 QY 62 KITEIDGDFPKLKNLHAILVNNKISKVSPGAFPLVLEKLYLSKNOLKEIPKMPKT 121
 DB 92 KITEIDGDFPKLKNLHAILVNNKISKVSPGAFPLVLEKLYLSKNOLKEIPKMPKT 151
 QY 122 LQELRAHEHETKRVKVTENGNNOMVIELGTNPLKSSGIGENGAFOGKKLSYIRADNN 181
 DB 152 LQELRAHEHETKRVKVTENGNNOMVIELGTNPLKSSGIGENGAFOGKKLSYIRADNN 211
 QY 182 ITSIPQGLPSPSLTEHLHDGKISRVDASLKGILNLAQGLSFNSISAVDNGSLANTPH 241
 DB 212 ITSIPQGLPSPSLTEHLHDGKISRVDASLKGILNLAQGLSFNSISAVDNGSLANTPH 271
 QY 242 RELHLDNNKLTTRVPGGLAHEKTYQVYLLHNNNISVVGSSDFPCPGHNTKASYSVGLS 301
 DB 272 RELHLDNNKLTTRVPGGLAHEKTYQVYLLHNNNISVVGSSDFPCPGHNTKASYSVGLS 331
 QY 302 NPQVWEIOPSTRCYVRSALQGLNYK 329
 DB 332 NPQVWEIOPSTRCYVRSALQGLNYK 359

RESULT 2
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 N:Alternate names: dermatan sulfate proteoglycan II; proteoglycan core protein II
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #ext_change 20-Aug-1999
 C:Accession: S06280; B31430; A26545; A20935
 R:Day, A.A.; McQuillan, C.I.; Termine, J.D.; Young, M.R.
 B:Chem. J. 248, 801-805, 1987
 A>Title: Molecular cloning and sequence analysis of the cDNA for small proteoglycan II
 A:Reference number: S06280; PMID:88133946; PMID:3435485
 A:Accession: S06280
 A:Molecule type: mRNA
 A:Residues: 1-360 <DAY>
 A:Cross-references: EMBL:Y00712; NID:G618; PDB:CAA6702.1; PID:G619
 A:Experimental source: bone
 R:Choi, H.U.; Johnson, T.L.; Pal, S.; Tang, L.H.; Rosenberg, L.; Neame, P.J.
 J. Biol. Chem. 264, 2876-2884, 1989
 A>Title: Characterization of the dermatan sulfate proteoglycans, DS-PGI and DS-PGII, fro
 A:Reference number: A31430; PMID:89123388; PMID:2914936
 A:Accession: B31430
 A:Molecule type: protein

A:Residues: 31-33,'X',35-54 <CHO>
 A:Experimental source: cartilage; fetal skin
 R:Coester, L.; Rosenberg, L.C.; van der Rest, M.; Poole, A.R.
 J. Biol. Chem. 262, 3809-3812, 1987
 A>Title: The dermatan sulfate proteoglycans of bovine sclera and their relationship t
 A:Reference number: A26545; PMID:87137687; PMID:3818667
 A:Accession: A26545
 A:Molecule type: protein
 A:Residues: 31-50 <COS>
 A:Experimental source: sclera
 R:Pearson, C.H.; Winterbottom, N.; Packre, D.S.; Scott, P.G.; Carpenter, M.R.
 J. Biol. Chem. 258, 15101-15104, 1983
 A:Reference number: A20935; PMID:84087911; PMID:6654908
 A:Accession: A20935
 A:Molecule type: protein
 A:Residues: 31-54 <PEA>
 A:Experimental source: skin
 R:Chopra, R.K.; Pearson, C.H.; Pringle, G.A.; Packre, D.S.; Scott, P.G.
 Biochem. J. 232, 277-279, 1985
 A>Title: Dermatan sulphate is located on serine-4 of bovine skin proteodermatan sulpi
 nces around glycosylation sites in different proteoglycans.
 A:Reference number: A44700; PMID:86103195; PMID:3936484

A:Contents: annotation; glycosylation
 C:Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglyc
 C:Keywords: Chondroitin sulfate proteoglycan; collagen binding; dermatan sulfate; ext
 F:1-15/Domains: signal sequence #status predicted <SIG>
 F:16-30/Domains: proteoglycan #status predicted <PRO>
 F:31-360/Product: decorin #status predicted <MAT>
 F:49-73/Domains: proteoglycan amino-terminal homology <PAH>
 F:83-106/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F:107-130/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:131-151/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F:152-175/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
 F:176-199/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
 F:202-222/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
 F:223-246/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
 F:247-270/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
 F:271-293/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
 F:294-308/Domains: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
 F:309-360/Domains: proteoglycan carboxyl-terminal homology <PC>
 F:34/Binding site: dermatan sulfate (Ser) (covalent) #status experimental
 F:190,326/Binding site: dermatan sulfate (Ser) (covalent) #status predicted
 F:212,263,304/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 91.3%; Score 1564.5; DB 2; Length 360;
 Best Local Similarity 89.7%; Pred No. 3, 7e-107; Indels 3; Gaps 2;
 Matches 296; Conservative 19; Mismatches 12;
 QY 2 EASGIGPE--VDDHDFPSPGAPVPCFPCQCHLRVQCSDDLGLKVPDLPPDTLLDLDQ 59
 DB 32 EASGIGPEHDFPSPGAPVPCFPCQCHLRVQCSDDLGLKVPDLPPDTLLDLDQ 90
 QY 60 NKKITEIDGDFPKLKNLHAILVNNKISKVSPGAFPLVLEKLYLSKNOLKEIPKMP 119
 DB 91 NKKITEIDGDFPKLKNLHAILVNNKISKVSPGAFPLVLEKLYLSKNOLKEIPKMP 150
 QY 120 KTLQELRAHEHETKRVKVTENGNNOMVIELGTNPLKSSGIGENGAFOGKKLSYIRAD 179
 DB 151 KTLQELRAHEHETKRVKVTENGNNOMVIELGTNPLKSSGIGENGAFOGKKLSYIRAD 210
 QY 180 TNSITPQGLPSPSLTEHLHDGKISRVDASLKGILNLAQGLSFNSISAVDNGSLANTP 239
 DB 211 TNSITPQGLPSPSLTEHLHDGKISRVDASLKGILNLAQGLSFNSISAVDNGSLANTP 270
 QY 240 HRELHLDNNKLTTRVPGGLAHEKTYQVYLLHNNNISVVGSSDFPCPGHNTKASYSVGL 299
 DB 271 HRELHLDNNKLTTRVPGGLAHEKTYQVYLLHNNNISVVGSSDFPCPGHNTKASYSVGL 330
 QY 300 FANPQVWEIOPSTRCYVRSALQGLNYK 329
 DB 331 FANPQVWEIOPSTRCYVRSALQGLNYK 360

RESULT 3

147020

decorin - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 20-Aug-1999

C/Accession: 147020

R/Zhan, Q.; Burrows, R.; Cincron, C.

Invest. Ophthalmol. Vis. Sci. 36, 206-215, 1995

A>Title: Cloning and in situ hybridization of rabbit decorin in corneal tissues.

A/Reference number: 147020; PMID:95122319; PMID:7822148

A/Accession: 147020

A/Molecule type: mRNA

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Cross-references: GB:S76584; NID:g913374; PIDN:AA33083.1; PID:g913375

C/Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan

F/49-73/Domain: leucine-rich alpha-2-glycoprotein repeat homology <PCH>

F/83-106/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F/107-130/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F/133-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F/152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>

F/176-199/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>

F/202-222/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>

F/223-246/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

F/247-270/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>

F/271-293/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>

F/294-308/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>

F/309-360/Domain: proteoglycan carboxyl-terminal homology <PCH>

Query Match 91.3%; Score 1564.5; DB 2; Length 360;

Best Local Similarity 90.6%; Pred. No. 3.7e-107;

Matches 299; Conservative 17; Mismatches 11; Indels 3; Gaps 2;

QY 2 EASGIGPR-VDDRDFPSLGPVCPFRQCHLRVQCSDLGDKPKLPPTTLIDIQ 59

DB 32 EASGIGPRABELPDL-D-MLGPVCPFRQCHLRVQCSDLGDKPKLPPTTLIDIQ 90

QY 60 NKKTEIKDGFKNLKNLALILVNNKISKVSPGATPLVKERLYLSKNOLKEPKNP 119

DB 91 NKKTEIKDGFKNLKNLALILVNNKISKVSPGATPLVKERLYLSKNOLKEPKNP 150

QY 120 KTLQELRAHENEITKRVKTYFNGLNOMIVIEGTNPGLKSSGIENGAFOGKKLSYRIADT 179

DB 151 KTLQELRAHENEITKRVKTYFNGLNOMIVIEGTNPGLKSSGIENGAFOGKKLSYRIADT 210

QY 180 TWITISIPQGLPSLTLEHLDGNKISRVDASLKLNNLAKLGLSFNSISAVNGSLANTP 239

DB 211 TWITISIPQGLPSLTLEHLDGNKISRVDASLKLNNLAKLGLSFNSISAVNGSLANTP 270

QY 240 HLRHLDNNKLTFRVGGIAEHKTYIOVYLLHNNNISVSSSDPCPPGHNTKASYSVSL 299

DB 271 HLRHLDNNKLTFRVGGIAEHKTYIOVYLLHNNNISVSSSDPCPPGHNTKASYSVSL 330

QY 300 FSNPVQWEIOPSTFRQCVVRSALIQGNK 329

DB 331 FSNPVQWEIOPSTFRQCVVRSALIQGNK 360

RESULT 4

S24317

decorin precursor - chicken

N/Alternate names: corneal chondroitin/dermatan sulfate proteoglycan

C/Species: Gallus gallus (chicken)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999

C/Accession: S24317; S58474; S22197

R/Li, W.; Vergnes, J.P.; Cornuet, P.K.; Hassell, J.R.

Arch. Biochem. Biophys. 296, 190-197, 1992

A>Title: cDNA clone to chick corneal chondroitin/dermatan sulfate proteoglycan reveals

A/Reference number: S24317; PMID:9229675; PMID:1605630

A/Accession: S24317

A/Molecule type: mRNA

A/Status: preliminary

A/Cross-references: EMBL:X63797; NID:g62887; PIDN:CAA45318.1; PID:g62888

A/Accession: S58474

A/Molecule type: protein

A/Residues: 31-33, 'X', 35-39, 'X', 41-48, 'X', 50-51 <LTA>

C/Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglyca

C/Keywords: collagen binding; extracellular matrix; glycoprotein

F/1-16/Domain: signal sequence #status predicted <SIG>

F/17-30/Domain: propeptide #status predicted <PRO>

F/31-357/Product: decorin #status experimental <MAT>

F/46-70/Domain: proteoglycan amino-terminal homology <PCH>

F/80-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F/104-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F/128-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F/149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>

F/173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>

F/199-219/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>

F/220-243/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

F/244-267/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>

F/268-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>

F/291-305/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>

F/306-357/Domain: proteoglycan carboxyl-terminal homology <PCH>

Query Match 82.6%; Score 1415; DB 2; Length 357;

Best Local Similarity 80.2%; Pred. No. 3.3e-96;

Matches 264; Conservative 28; Mismatches 37; Indels 0; Gaps 0;

QY 1 VEASGIGPRVDDRDFPSLGPVCPFRQCHLRVQCSDLGDKPKLPPTTLIDIQ 60

DB 29 IEDESSADMAPPTDDVISGFGVCPFRQCHLRVQCSDLGDKPKLPPTTLIDIQ 88

QY 61 NKKTEIKDGFKNLKNLALILVNNKISKVSPGATPLVKERLYLSKNOLKEPKNP 120

DB 89 NKKTEIKDGFKNLKNLALILVNNKISKVSPGATPLVKERLYLSKNOLKEPKNP 148

QY 121 TLQELRAHENEITKRVKTYFNGLNOMIVIEGTNPGLKSSGIENGAFOGKKLSYRIADT 180

DB 149 TLQELRAHENEITKRVKTYFNGLNOMIVIEGTNPGLKSSGIENGAFOGKKLSYRIADT 208

QY 181 NTSITIPQGLPSLTLEHLDGNKISRVDASLKLNNLAKLGLSFNSISAVNGSLANTP 240

DB 209 NTSITIPQGLPSLTLEHLDGNKISRVDASLKLNNLAKLGLSFNSISAVNGSLANTP 268

QY 241 LRLHLDNNKLTFRVGGIAEHKTYIOVYLLHNNNISVSSSDPCPPGHNTKASYSVSL 300

DB 269 LRLHLDNNKLTFRVGGIAEHKTYIOVYLLHNNNISVSSSDPCPPGHNTKASYSVSL 328

QY 301 FSNPVQWEIOPSTFRQCVVRSALIQGNK 329

DB 329 FSNPVQWEIOPSTFRQCVVRSALIQGNK 357

RESULT 5

A55454

decorin precursor - mouse

N/Alternate names: proteoglycan II

C/Species: Mus musculus (house mouse)

C/Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 20-Aug-1999

C/Accession: A55454; S20812

R/Scholz, T.; Solursh, M.; Suzuki, S.; Reiter, R.; Morgan, J.L.; Buchberg, A.M.; Sir

J. Biol. Chem. 269, 28270-28281, 1994

A>Title: The murine decorin. Complete cDNA cloning, genomic organization, chromosomal

A/Reference number: A55454; PMID:9505610; PMID:7961765

A/Accession: A55454

A/Molecule type: mRNA

A/Status: preliminary

A/Cross-references: GB:S53929; NID:g53668; PIDN:CAA37876.1; PID:g53669

R/Natoli, Y.; Suzuki, S.

Submitted to the EMBL Data Library, July 1990

A/Description: Nucleotide sequences of cDNAs encoding mouse PGI and PGI1.

A/Reference number: S20812

A/Accession: S20812

A/Molecule type: mRNA

F/161-184/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK4>
F/185-208/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK3>
F/210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK2>
F/231-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK1>
F/255-278/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK0>
F/279-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK3>
F/302-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK4>
F/317-369/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK5>
F/421-48,181,199/Binding site: dermatan sulfate (Ser) (covalent) #status predicted
F/427,312/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 57.5%; Score 985.5; DB 2; Length 369;
Best Local Similarity 57.6%; Pred. No. 1e-64;
Matches 190; Conservative 51; Mismatches 86; Indels 3; Gaps 2;

QY 2 EASGIGPE--VPDDDFEPLSGVPCFPCQCHLRVQCSDLGLDKVPKDLPTDTLLDQ 59
DB 40 EASGSDTTSQVDDLSVTPFSAMCFPGCHLRVQCSDLGLKVPKXISPDITLLDQ 99

QY 60 NKKITEIKDGDFKNTKNTLHALILVNNKISKVSPGAFPLVLELYLSRNQKELPEKMP 119
DB 100 NNDISELRKDDPKGLOHLYALVNNKISKIHEKAFSPRLKQKLYISQNHVEIPNLP 159

QY 120 KTLQELRAHENEITKRYKTENGINOMVIEIGTNPFLKSSGIEENGAFQMKLSYRIAD 179
DB 160 SSLVELRIDHNRIRKVPKGVFSGLRNMNCIEWGPNLENSGEPGAFDGL-KLNTYLRISE 218

QY 180 TMTISIPQGLPSSLTEIHDGKIKISRVDAASLKGILNNTAKLGSFNSISAVNGSLAMP 239
DB 219 AKLTGIPKDLPTLWELHLDHNKIQALEDLIRYSKYLRLGHNQIMTIENGSLFIP 278

QY 240 HRLRLHDNNKLTTRVPGGLAEHKYIQVYLIANNISVSGSDPCPGHNTKASYSGVSL 299
DB 279 TLRLHLHDNNKLSRPVAGLPDLKLTQVYLIHNSNITKVGINDPCPGFVKAYNYGISL 338

QY 300 FSNPVQYWEIOPSTFRVCYVRSALIOGNKY 329
DB 339 FNNPVYWEVQPATFRCTVDRALIOGNKY 368

RESULT 8
S20811
Proteoglycan I - mouse
N/Alternate names: biglycan
C/Species: Mus musculus (house mouse)
C/Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #ext_change 20-Aug-1999
C/Accession: S20811; A57645; I49534
R/Author: Y. Suzuki, S. submitted to the EMBL Data Library, July 1990
A/Description: Nucleotide sequences of cDNAs encoding mouse PGI and PGI1.
A/Reference number: S20811
A/Accession: S20811
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-369 <NAI>
A/Accession: S20811; NID:953666; PIDN:CAA37875.1; PID:953667
R/Wegrowski, Y.; Pilliarsetti, J.; Danielson, K.G.; Suzuki, S.; Iozzo, R.V.
Genomics 30, 8-17, 1995
A/Title: The murine biglycan: complete cDNA cloning, genomic organization, promoter function
A/Reference number: A57645; MUID:9612925; PMID:8595907
A/Accession: A57645
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-67, 'W', 69-369 <WEG>
A/Cross-references: GB:L02076; NID:9348961; PIDN:AAA64360.1; PID:9348962
A/Note: authors translated the codon TGG for residue 58 as Cys
R/Kau, W.; Just, W.; Vetter, U.; Vogel, W.
Mamm. Genome 5, 395-396, 1994
A/Title: A dinucleotide repeat in the mouse biglycan gene (BST) on the X chromosome.
A/Reference number: I49534; MUID:94319093; PMID:8043360
A/Accession: I49534
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA

A/Residues: 1-67, 'W', 69-369 <RES>
A/Cross-references: GB:L02076; NID:9348961; PIDN:AAA64360.1; PID:9348962
C/Genetics:
A/Genes: Bgn
C/Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan
C/Keywords: chondroitin sulfate, proteoglycan, dermatan sulfate, extracellular matrix;
F/58-82/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK1>
F/92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK2>
F/116-139/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK3>
F/140-160/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK4>
F/161-184/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK5>
F/185-208/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK6>
F/210-230/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK7>
F/231-254/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK8>
F/255-278/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK9>
F/279-301/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK0>
F/302-316/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK1>
F/317-369/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRK2>

Query Match 57.5%; Score 984.5; DB 2; Length 369;
Best Local Similarity 57.6%; Pred. No. 1.2e-64;
Matches 190; Conservative 51; Mismatches 86; Indels 3; Gaps 2;

QY 2 EASGIGPE--VPDDDFEPLSGVPCFPCQCHLRVQCSDLGLDKVPKDLPTDTLLDQ 59
DB 40 EASGSDTTSQVDDLSVTPFSAMCFPGCHLRVQCSDLGLKVPKXISPDITLLDQ 99

QY 60 NKKITEIKDGDFKNTKNTLHALILVNNKISKVSPGAFPLVLELYLSRNQKELPEKMP 119
DB 100 NNDISELRKDDPKGLOHLYALVNNKISKIHEKAFSPRLKQKLYISQNHVEIPNLP 159

QY 120 KTLQELRAHENEITKRYKTENGINOMVIEIGTNPFLKSSGIEENGAFQMKLSYRIAD 179
DB 160 SSLVELRIDHNRIRKVPKGVFSGLRNMNCIEWGPNLENSGEPGAFDGL-KLNTYLRISE 218

QY 180 TMTISIPQGLPSSLTEIHDGKIKISRVDAASLKGILNNTAKLGSFNSISAVNGSLAMP 239
DB 219 AKLTGIPKDLPTLWELHLDHNKIQALEDLIRYSKYLRLGHNQIMTIENGSLFIP 278

QY 240 HRLRLHDNNKLTTRVPGGLAEHKYIQVYLIANNISVSGSDPCPGHNTKASYSGVSL 299
DB 279 TLRLHLHDNNKLSRPVAGLPDLKLTQVYLIHNSNITKVGINDPCPGFVKAYNYGISL 338

QY 300 FSNPVQYWEIOPSTFRVCYVRSALIOGNKY 329
DB 339 FNNPVYWEVQPATFRCTVDRALIOGNKY 368

RESULT 9
S32559
biglycan precursor - bovine
N/Alternate names: dermatan sulfate proteoglycan I (DS-PGI); proteochondroitin core p
C/Species: Bos primigenius taurus (cattle)
C/Date: 03-May-1994 #sequence revision 20-Feb-1995 #ext_change 07-May-1999
C/Accession: S32559; S34229; A31701; A31430; PT0078; S55673; A3137
R/Torok, M.A.; Evans, S.A.S.; Marcum, J.A.
Biochim. Biophys. Acta 1173, 81-84, 1993
A/Title: cDNA sequence for bovine biglycan (PGI) protein core.
A/Reference number: S32559; MUID:93250052; PMID:8485158
A/Accession: S32559
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-369 <TOR>
A/Cross-references: EMBL:L07953; NID:9162746
A/Experimental source: aortic smooth muscle
R/Marcum, J.A.; Torok, M.; Evans, S.
submitted to the EMBL Data Library, December 1992
A/Reference number: S34229
A/Accession: S34229
A/Molecule type: mRNA
A/Residues: 1-250 'V', 252-369 <MAR>
A/Cross-references: EMBL:L07953
R/Name, P.U.; Choi, H.U.; Rosenberg, L.C.
J. Biol. Chem. 264, 8653-8661, 1989

RESULT 13

A46743

luminan precursor - bovine

N/Alternate names: 37K keratan sulfate-linked protein; corneal keratan sulfate proteoglycan
C/Species: Bos primigenius taurus (cattle)
C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 24-Sep-1999

C/Accession: A46743; A53379

R/Funderburgh, J.L.; Funderburgh, M.L.; Brown, S.J.; Vergnes, J.P.; Hassell, J.R.; Mann, J. Biol. Chem. 268, 11874-11880, 1993

A/Title: Sequence and structural implications of a bovine corneal keratan sulfate proteoglycan

A/Reference number: A46743; PMID:93280153; PMID:8099356

A/Accession: A46743

A/Molecule type: mRNA

A/Residues: 1-342 <FNU>

A/Cross-references: GB:U11063; NID:9163266; PIDN:AAA30608.1; PID:9163267

A/Experimental source: cornea

R/Funderburgh, J.L.; Conrad, G.W.

J. Biol. Chem. 265, 8297-8303, 1990

A/Title: Isoforms of corneal keratan sulfate proteoglycan.

A/Reference number: A53379; PMID:90243714; PMID:2135877

A/Accession: A53379

A/Molecule type: protein

A/Residues: 19-36 <FNU>

A/Experimental source: cornea

C/Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology

C/Keywords: glycoprotein; tandem repeat

F1-18/Domain: signal sequence #status predicted <SIG>

F19-342/Product: luminan #status predicted <MAT>

F192,131,164,256/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.8%; Score 356.5; DB 2; Length 342;

Best Local Similarity 31.7%; Pred. No. 1,1e-18;

Matches 107; Conservative 57; Mismatches 143; Indels 31; Gaps 12;

QY 3 ASGIGPEVDDRDPEPSL---GPVCPFRCC---HLRVQCSDLGLDKVPEKDLPPDTTL 55

DB 16 ASSTPYDYEEYDFQALYGRSPRCAPCECPESYPSAMTCDEKLKSVPM-VPPGKY 74

QY 56 LDKQNKTEIKDGFQKLNLIHLYNNKI--SKVSPGAPFPLVLERLYLSKNOQKE 113

DB 75 LYLRNNOQIDHIDDKAFENVTLQWLIHNLNLENSKIKGVSKQKQKLIHNNLTLE 134

QY 114 LPEKPKTLOELRAHNEITVRYKKTFFNGLNQMIYIEGTPLKSSGLENAGFOGMKLS 173

DB 135 SVGPSPKSLVDQLTNNTKISLKG--SPDGLVNLFTFHLQHQLKEDAV-SALNGLKSLR 191

QY 174 YIRIADTVITSIPOGLPSELTEHLDGNKISRVDASLKGKLNIAKGLSFRNSI--SAVD 231

DB 192 YLDSFNMOTKLPSGLPVSLLTYLDNNKISINIPDEYKRSALQYLRLSHNELDASGVP 251

QY 232 NGSLANTPHLEHLHDNNKLTFRVPGLAHEKRYIQVYLAHNNNISVSSSDPCP---PGHN 288

DB 252 GNSF-NVSSLELDLSYKLSIP---TVNENLENYLEVNELEFVDKSCXKILGP--- 304

QY 289 TKKASYSQVS---LFSNPVQWEIOPSTFRCVYRSAL 323

DB 305 ---LSYSKIKHLRDLGNHITQTSLEPPDYECIRVANEI 339

RESULT 14

S52284

luminon, secretory interstitial proteoglycan precursor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 24-Sep-1999

C/Accession: S52284

R/Krull, N.B.

submitted to the EMBL Data Library, January 1995

A/Reference number: S52284

A/Accession: S52284

A/Status: Preliminary

A/Molecule type: mRNA

A/Residues: 1-338 <KRU>

A/Cross-references: EMBL:X84039; NID:9643023; PIDN:CAA58858.1; PID:9643024

C/Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology

Query Match 20.3%; Score 347.5; DB 2; Length 338;

Best Local Similarity 31.5%; Pred. No. 5,1e-18;

Matches 100; Conservative 56; Mismatches 134; Indels 27; Gaps 11;

QY 20 LGPVCPRCC---HLRVQCSDLGLDKVPEKDLPPDTTLDLQNNKTEIKDGFQKLN 76

DB 33 LSPVCAECNCPHSYPTAMCDDDLKLSVPM-VPPGKYLYLRNNOIDHIDDKAFENVTD 91

QY 77 LHALILVNNKI--SKVSPGAPFPLVLERLYLSKNOQKEPEKPKTLOELRAHNEITK 134

DB 92 LQWLIHNLNLENSKIKGVSKQKQKLIHNNLTESVGPLKSLQDLQNNKISK 151

QY 135 VRKTYFNGLNQMIYIEGTPLKSSGLENAGFOGMKLSYIRIADTVITSIPOGLPSEL 194

DB 152 LG--SPDGLVNLFTFHLQHQLKEAV-SASLKLKSLLEYLDLSFNGMSKLPALPISL 208

QY 195 ELHLDGNKISRVDASLKGKLNIAKGLSFRNSI--SAVDNGSLANTPHLEHLHDNNKLT 252

DB 209 TLYLDNNKLTIVIPDEYFNRFQGLQYLRLSHNELDASGVPGNSF-NISLLELDLSYNDLK 267

QY 253 RVPGGLAEHKYIQVYLAHNNNISVSSSDPCP---PGHNTKASYSQVS---LFSNPVQ 306

DB 268 SIP---TVNENLENYLEVNELEFVDKSCXKILGP-----LSYSKIKHLRDLGNPLTO 318

QY 307 WEIOPSTFRCVYRSAL 323

DB 319 SLPDPDYECIRVANEI 335

RESULT 15

slit-1 protein homolog - rat

N/Alternate names: MEK4 protein

C/Species: Rattus norvegicus (Norway rat)

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2002

C/Accession: T42218

R/Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.

Genomics 51, 27-34, 1998

A/Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs

A/Reference number: Z14126; PMID:98360089; PMID:9633030

A/Accession: T42218

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1531 <NAK>

A/Cross-references: EMBL:AB011530; NID:93449289; PIDN:BA32460.1; PID:93449290

A/Experimental source: strain Sprague-Dawley; Drain

C/Genetics:

C/Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein

Query Match 19.1%; Score 327.5; DB 2; Length 1531;

Best Local Similarity 24.9%; Pred. No. 1,2e-15;

Matches 96; Conservative 65; Mismatches 122; Indels 103; Gaps 9;

QY 10 VPDDRDF---EPSLGVCPFRCCCHLRVQCSDLGLDKVPEKDLPPDTTLDLQNNKITE 65

DB 495 IPTGDEYHNSSECTSDVACPHKCRCEASVYECGGLKSKIPERIPSTTELRANNEISI 554

QY 66 IK-DGDFKLNKLIHALILVNNKISKVSPPGAPFPLVLERLYLSKNOQKEPEKPKTLOE 124

DB 555 LEATGTFKPKLSHKKLNINNNKYSLEIDGTFEGATSESHLTPANQLESVSGWFRGLDG 614

QY 125 LRA---HENETVRYKKTFFNGLNQMIYIEGTPLKSSGLENAGFOGMKLS----- 173

DB 615 LRTLMNNRISICHNDSFTGLRNVRLLSLYDNHITT--ISPPAFDTQLALSTLNLAMP 672

QY 174 ----- 173

DB 673 FNCNQLAWLWLRKKKTYTGNPQGNPDPFLAQIPLQDVAFPDFRCEBGEVGCILRP 732

QY 174 -----YIRADTNTISIPQGLPSLTETLHLDGNKISRVDAAASIKGLNNTLAKGL 222
 Db 733 QCPQACADIVYRCNKHGLPKGIPKNNVELYDNGQFTLV-PGQSTFKYIQVLDL 791
 QY 223 SFNSISAVDNGSLANTPHILREHLDDNNKLTREV---GGLAHHKTYQVYLLHNNNISVGG 278
 Db 792 SNNKISSLSNSSFMTWMSQLTLLTSLYNALQICIPPLAQGL---RSIRLHLSHGNDVSTLQ 848
 QY 279 SSDPCPGRHNTKKASYSYGSVLSFSPNPV 304
 Db 849 EGIF-----ADVTSLSHLAGANPL 868

RESULT 16

T13953
 MEGF5 protein - rat
 N:Alternate names: slit protein homolog
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 16-Aug-2002
 C:Accession: T13953
 R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
 Genomics 51, 27-34, 1998
 A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
 A:Reference number: Z14126; MUID:98360089; PMID:9693030
 A:Accession: T13953
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-153 <NAK>
 A:Cross-references: EMBL:AB011531; NID:G3449291; PIDN:BAA32461.1; PID:G3449292
 C:Genetics:
 A:Gene: MEGF5
 C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein
 Query Match 19.1%; Score 327; DB 2; Length 1523;
 Best Local Similarity 24.9%; Pred. No. 1.3e-15;
 Matches 99; Conservative 53; Mismatches 124; Indels 122; Gaps 7;
 QY 21 GP---VCPRCOCHLAVVQCSDLGDKVPKDLPPDTLLDQNNKTEIKDGPFKYKLN 77
 Db 28 GPPAAACPTKCTCSAASVDCGHLGLRAVPRGIPRNARRLDLDNNNTTRITKMPFTGLKNL 87
 QY 78 HALIVNNKISKVSPGAFPLVLEKRLYLSKNQLEKPEKM---PRTYQELRAHNEIT 133
 Db 88 RVHLIEDNQSVIERGAFQDLKLERLRANKLQVLPPELLPOSTRK-LTRLDLSNQIQ 146
 QY 134 KVRKVTENGINQMIIVIELGTPNPKSSGIENGAFQGMKKLSYIRADNTI----- 182
 Db 147 GIPKAFRGVYGVKNQLDNNHI--SCIEDGAFRALDLEILTLNNNNISRIILVTSFNM 204
 QY 183 ----- 182
 Db 205 PKIRTRLHSLNHLVCDCHLAWLSDWLRQRRTTIGQFTLCMAVHLRGFSVADVQKKEVCP 264
 QY 183 -----TSIPQGLPSLTETLHLDGNKISRVD 208
 Db 265 GRHSEAPACVANSLSGCSAASCSNNIVDCGKGLTEIPALPEGIVAIRLEQSSISIPA 324
 QY 209 ASIKGLNNTLAKGLSFNSISAVDNGSLANTPHILREHLDDNNKLTREVGLAHHKY-IQVV 267
 Db 325 GAFIQYKRLKRIDISKQISDIAADAFQGLKSLTSLVYGNKITEIPKGLFDGLVSLQL 384
 QY 268 YLENNNISVVGSSDFCPGRHNTKKASYSYGSVLSFSPNPV 305
 Db 385 LTNANKINCLRVTF-----QDLQNLINLISLYDNKIQ 416

RESULT 17

S55275
 fibromodulin precursor - human
 N:Alternate names: 59K collagen-binding matrix protein
 C:Species: Homo sapiens (man)
 C>Date: 23-Aug-1995 #sequence_revision 03-Oct-1995 #text_change 24-Sep-1999
 C:Accession: S55275; S35710; S32752; S41925

R:Hildebrand, A.; Romaris, M.; Rasmussen, L.M.; Heinegard, D.; Twardzik, D.R.
 Biochem. J. 302, 527-534, 1994
 A:Title: Interaction of the small interstitial proteoglycans biglycan, decorin and fib
 A:Reference number: S55275; MUID:94379985; PMID:8093006
 A:Accession: S55275
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-376 <H12>
 A:Cross-references: EMBL:X75546; NID:G453156; PIDN:CAA53233.1; PID:G453157
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
 R:Antonsson, P.; Heinegard, D.; Oldberg, A.
 Biochim. Biophys. Acta 1174, 204-206, 1993
 A:Title: Structure and deduced amino acid sequence of the human fibromodulin gene.
 A:Reference number: S35710; MUID:93363641; PMID:8357838
 A:Accession: S35710
 A:Molecule type: DNA
 A:Residues: 1-3, 'T', '5'-86, 'P', '88-209, 'N', '211-225, 'Y', '227-343, 'Q', '345-354, 'W', '356-362, 'I
 A:Cross-references: EMBL:X72913; NID:G297090; PIDN:CAA51418.1; PID:G297091
 C:Comment: Keratan sulfate can be covalently attached to N-acetylglucosamine at the a
 C:Genetics:
 A:Gene: GDB:PMOD
 A:Cross-references: GDB:228979; OMIM:600245
 A:Map position: 1q32.1-1q32.1
 A:Insertions: 326/2
 C:Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology
 C:Keywords: cartilage; chondroitin sulfate proteoglycan; collagen binding; connective
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-376/Product: fibromodulin #status predicted <MAT>
 F:8,39,42,45,47,50,53,55,63,65/Binding site: sulfate (tyr) (covalent) #status predict
 F:127,166,201,291/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 19.1%; Score 326.5; DB 2; Length 376;
 Best Local Similarity 27.9%; Pred. No. 2.1e-16;
 Matches 91; Conservative 64; Mismatches 146; Indels 25; Gaps 8;

QY 8 PEVDDRDPEPSLGVCPFCOC---HLRVQCSDLGDKVPKDLPPDTLLDQNNKIT 64
 Db 68 PSPDPDRD-----CPQECDCPPNPLFAMVCDNRNKLKLP-FVPSRMKYVYFQNGQT 118
 QY 65 EIKDGFQKULHALLIVNNKIS--KSPGAFPLVLEKRLYLSKNQLEKPEKPKTL 122
 Db 119 SIOGVDFDVGTLMTALHGNQITSDKVRKYFSKIRHERLYLDNNITRMPGPRSL 178
 QY 123 QELRAHNEITVYKRTFNGMIVIELGTPNPKSSGIENGAFQGMKKLSYIRADNTI 182
 Db 179 RELHLDHNOISRVNNALEGLNLTALVYQHDIEQVG--SSMRGLRSLILDLDSYNIH 235
 QY 183 TSIPQGLPSLTETLHLDGNKISRVDAAASIKGLNNTLAKGLSFNSISAVDNGSLANT---P 239
 Db 236 RKVPDGLPSALDGLVMEHNNVYTPDSYFRGAPKLLVYVLSNLSL--NNGLASNTFNS 293
 QY 240 HREHLDDNNKLTREVGLAHHKYIQVYLLHNNNISVVGSSDFCPGRHNTKKASYSVSL 299
 Db 294 SLLELDLSYNQLOKTP---PVNTLENTLYQGRINEFSSFCYVADVNVNSKQVYRL 350
 QY 300 FSNPVOYWEIQPSTFRCYVYRSLIQ 325
 Db 351 DGENEIRSAMPADAPICLRSLSTET 376

RESULT 18

B36665
 slit protein 2 precursor - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002
 C:Accession: B36665
 R:Rothenberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Aravanis-Tsakonas, S.
 Genes Dev. 4, 2169-2187, 1990
 A:Title: slit: an extracellular protein necessary for development of midline glia and
 A:Reference number: A36665; MUID:91099665; PMID:2176636
 A:Accession: B36665
 A:Status: preliminary
 A:Molecule type: mRNA

A/Residues: 1-1469 <ROT>
A/Cross-references: GB:X53959
C/Genetic8:
A/Genes: FlyBase:sl1
A/Cross-references: FlyBase:FBgn0003425
C/Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein
F/66-91/Domain: proteoglycan amino-terminal homology <PAH1>
F/101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F/125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F/149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F/173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F/197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F/228-272/Domain: proteoglycan amino-terminal homology <PAH2>
F/323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F/347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F/371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F/395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
F/419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F/450-494/Domain: proteoglycan amino-terminal homology <PAH3>
F/512-537/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F/547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F/572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F/620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F/651-695/Domain: proteoglycan amino-terminal homology <PAH4>
F/708-733/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F/743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F/767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F/846-890/Domain: proteoglycan amino-terminal homology <PAH5>
F/1028-1061/Domain: EGF homology <EGF1>
F/1068-1099/Domain: EGF homology <EGF2>
F/1115-1148/Domain: EGF homology <EGF1>

Query Match 18.9%; Score 323; DB 2; Length 1469;
Best Local Similarity 25.3%; Pred. No. 2,4e-15;
Matches 99; Conservative 61; Mismatches 129; Indels 102; Gaps 9;
2 EASGIGPEVDDDRFSPSLGVCPPRCQCHLRVQSGDLGDKVPKDLPPDTLLDLDLQNN 61
277 KCSGLTEHAPMECGAENS-----CPHRCADGIVDCREKSLTSVPVTLPPDTTIDVRLQON 332
62 KITTEIKDGFKNLKNLHALLIVNNKISKVSFGAFTPLVLERLYLSKNQKLEPERKPKT 121
333 FITELPKKSFSSFRRLRRIDLSNNNISRIADHLSGLKQTLTVLVGNKKIDLPSSGVFKG 392
122 LOELR---AHENETTKRKTYFNGLNQMTIVIELGTNPLKSSGIGENGAFOGKKLSYRIA 178
393 LGSIRLLILNANETISCTIRKDAFRDLHSLSLSLYDNNIQS--LANGTFDMKSMKTVHLA 450
179 -----DTN----- 181
451 KNPIFCNLRWLADYLHKNPITSGARCESPKRMHRRRIEELREKFKCSWGELRMKLS 510
182 -----ITSIPQGLPSPILTEHLIDGNKISRVDASLNG-L 214
511 GECRMDSDCPAMGCHGCTVYDCTGRKLEIPRDIPLHTTELLANDNLGHSISGLGRLL 570
215 NNIAKGLGSRISIAVNGSLANTPHLRRLHLDNNKLTTRVPGG--LAEHKTYQVVIYANN 272
571 PHLVKELKRNQQLTGIEPNFEGASHIQELQGENKIKESINRKFGLHQ-LKTINLYDN 629
273 NISVAGSSDFCPGPHNTKKASYSGLSPNSP 303
630 QIGCV-----MPGSFHLNLSITSLNLSNP 654

RESULT 19
A36665
slit protein 1 precursor - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002
C/Accession: A36665; A31640; S13523

R/Rothberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A/Title: slit: an extracellular protein necessary for development of midline glia and
A/Reference number: A36665; PMID:91099665; PMID:2176636
A/Accession: A36665
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1480 <ROT>
A/Cross-references: GB:X53959; NID:98614; PID:CA937910.1; PID:98615
R/Rothberg, J.M.; Hartley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.
Cell 55, 1047-1059, 1988
A/Title: slit: An EGF-homologous locus of D. melanogaster involved in the development
A/Reference number: A31640; PMID:8907553; PMID:314436
A/Accession: A31640
A/Molecule type: DNA
A/Residues: 861-1182, 'G', '1185-1404', 'GT', '1463-1464', 'YHA' <RO2>
A/Cross-references: GB:W23543; NID:9340939; PID:9514357
C/Genetic8:
A/Genes: FlyBase:sl1
A/Cross-references: FlyBase:FBgn0003425
A/Intons: 1351/3
C/Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein
C/Keywords: alternative splicing; growth factor
F/66-91/Domain: proteoglycan amino-terminal homology <PAH1>
F/101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F/125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F/149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F/173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F/197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F/228-272/Domain: proteoglycan amino-terminal homology <PAH2>
F/323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F/347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F/371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F/395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
F/419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F/450-494/Domain: proteoglycan amino-terminal homology <PAH3>
F/512-537/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F/547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F/572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F/620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F/651-695/Domain: proteoglycan amino-terminal homology <PAH4>
F/708-733/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F/743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F/767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F/846-890/Domain: proteoglycan amino-terminal homology <PAH5>
F/1028-1061/Domain: EGF homology <EGF1>
F/1068-1099/Domain: EGF homology <EGF2>
F/1115-1148/Domain: EGF homology <EGF1>

Query Match 18.9%; Score 323; DB 2; Length 1480;
Best Local Similarity 25.3%; Pred. No. 2,4e-15;
Matches 99; Conservative 61; Mismatches 129; Indels 102; Gaps 9;
2 EASGIGPEVDDDRFSPSLGVCPPRCQCHLRVQSGDLGDKVPKDLPPDTLLDLDLQNN 61
277 KCSGLTEHAPMECGAENS-----CPHRCADGIVDCREKSLTSVPVTLPPDTTIDVRLQON 332
62 KITTEIKDGFKNLKNLHALLIVNNKISKVSFGAFTPLVLERLYLSKNQKLEPERKPKT 121
333 FITELPKKSFSSFRRLRRIDLSNNNISRIADHLSGLKQTLTVLVGNKKIDLPSSGVFKG 392
122 LOELR---AHENETTKRKTYFNGLNQMTIVIELGTNPLKSSGIGENGAFOGKKLSYRIA 178
393 LGSIRLLILNANETISCTIRKDAFRDLHSLSLSLYDNNIQS--LANGTFDMKSMKTVHLA 450
179 -----DTN----- 181
451 KNPIFCNLRWLADYLHKNPITSGARCESPKRMHRRRIEELREKFKCSWGELRMKLS 510


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QY 182 -----ITSIPQGLPPSLTRELHLDGNKISRVDAAALSLK-L 214
DB 511 GECRMDSDCPAMCHCCTTVDCTGRKLEIPRIDPLHTTELLANDELGISSDGLFGRK 570
QY 215 NNIAKLGISFNSISAVDNGSLANTPHIRELHLDNNKLTVPFGS--DAEHKYIQVYLVHNN 272
DB 571 PHLVKELKRNQUTGIEBPNAFEGASHIQELQGENIKKISNMFGILMQ-LKTALVLYNN 629
QY 273 NISVVGSSDFCPFGHNTKKAISYGSVLSFNSP 303
DB 630 QISCV-----MGSFEHLNLSLTSLNLSNP 654

RESULT 20
S05390
Fibromodulin precursor - bovine
N:Alternate names: 59k collagen-binding matrix protein
C:Species: Bos primigenius taurus (cattle)
C:Date: 22-Jan-1993 #sequence revision 22-Jan-1993 #text_change 24-Sep-1999
C:Accession: S05390; S26942; S06040
R:Olderg, A.; Antomson, P.; Lindblom, K.; Heinegard, D.
EMBO J. 8, 2601-2604, 1989
A:Title: A collagen-binding 59-kd protein (fibromodulin) is structurally related to the
A:Reference number: S05390; PMID:9060020; PMID:2531085
A:Accession: S05390
A:Molecule type: mRNA
A:Residues: 1-375 <OLD>
A:Cross-references: GB:X16485; EMBL:X16305; NID:g353; PIDN:CA034503.1; PID:g354
A:Accession: S26942
A:Molecule type: protein
A:Residues: 90-105;190-199;274-281 <OLD>
R:Plaas, A.H.K.; Neame, P.O.; Niven, C.M.; Reiss, L.
J. Biol. Chem. 265, 20634-20640, 1990
A:Title: Identification of the keratan sulfate attachment sites on bovine fibromodulin.
A:Reference number: A23663; PMID:91056119; PMID:2243109
A:Contents: annotation; keratan sulfate attachment
C:Comment: Keratan sulfate can be covalently attached to N-acetylglucosamine at the aspa
C:Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology
C:Keywords: cartilage; chondroitin sulfate proteoglycan; collagen binding; connective ti
F:1-18/Domain: signal sequence #status predicted <Sig>
F:19-375/Product: fibromodulin #status experimental <MAT>
F:38-42,45,47,50,53,62,64/Binding site: sulfate (Tyr) (covalent) #status predicted
F:126,165,200,230/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 18.4%; Score 314.5; DB 2; Length 375;
Best Local Similarity 29.6%; Pred. No. 1.6e-15;
Matches 84; Conservative 55; Mismatches 120; Indels 25; Gaps 8;

QY 8 PEVPPDRDEPSPISGVPFCPRQC--HLRVQCSDLGLDKVPKDLPPDTLLDLONNKIT 64
DB 67 PQQPEPRD-----CPQECDCPPNFPPTAMYCDNNLTKLP-FVPSRMKYVVFQNNQIS 117
QY 65 EIKDGFKXKLNHALILVNNKIS--KVSQAFPLVKLERLYLSNQLKEPEKPKTL 122
DB 118 SIQEGFNDATGLIMLHGNQITSDVKVQKVSFKIRHRLTLHNNLTRLTSPRSKL 177
QY 123 QELRAHENEITKRVKVTNGLNOMVIELGTNPILKSSGIEGAFQGMKKLSYIRIADTN 182
DB 178 RELHLDHNGISRPNNALGLENLTALYLHNEIQGV--SSMKGLRSILDLDSYNH 234
QY 183 TSPQGLPSPSLTELHLDGNKISRVDAAALSLKLNNAKLGISFNSISAVDNGSLANT--P 239
DB 235 RKVPDELPSALTEQLYEHNNVFSPVPSYFGSPKLLYVRLSHNSLT--NNGLASNTFNS 292
QY 240 HLRELHLDNNKLTFRVPGGLAEHKYIQVYLVHNNNISVSSSDC 263
DB 293 SLLELDLSTNQLQKIP--PVTNLENTLYLQGNRINEFSISFC 333

RESULT 21
T42626
secreted leucine-rich repeat-containing protein SLIT2 - mouse (fragment)
N:Alternate names: neurogenic extracellular slit protein

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C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text_change 16-Aug-2002
C:Accession: T42626
R:Holmes, G.P.; Negus, K.; Burridge, L.; Raman, S.; Algar, E.; Yamada, T.; Little, M.;
Mech. Dev. 79, 57-72, 1998
A:Title: Distinct but overlapping expression patterns of two vertebrate slit homologs
A:Reference number: Z22177; PMID:99279228; PMID:10346621
A:Accession: T42626
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1025 <HOL>
A:Cross-references: EMBL:AF074960; NID:g4151258; PID:g4151259; PIDN:AAD04345.1
C:Genetics: Slit2
C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein;

Query Match 18.3%; Score 314; DB 2; Length 1025;
Best Local Similarity 25.4%; Pred. No. 6.7e-15;
Matches 100; Conservative 59; Mismatches 122; Indels 112; Gaps 11;

QY 24 CPFRQCHLRVQCSDLGLDKVPKDLPPDTLLDLONNKITEIK-DGDFKTLKLNHALIL 82
DB 2 CEPKCRCEGTVDSCSNQRLNKIPDHIPQYTAELRLNNEFTVLAAGIFKGLPQLRXINF 61
QY 83 VNNKISKVSPGAFPLVKLERLYLSNQLKEPEKPKTLQELRA----- 127
DB 62 SNKKTIDIEGAFEGASGVNEILTSNRLNVOHKMFKGLSLKTLMSNRISCVGND 121
QY 128 -----HENETKRVKVTNGLNOMVIELGTNP----- 155
DB 122 FIGLGSVRLSLYNDQITTVAGAPKXLSLSTNLNLANPNCNCHLAMELRRKRY 161
QY 156 -----IKSSGIEGAFQ-----GKKKLS-----YIRIADTN 182
DB 182 TGNPRCQCFYFLKEIPIDVVALQDPFCTDGDNDNSCSPSRPSECTCLDTYVRCNNKL 241
QY 183 TSPQGLPSPSLTELHLDGNKISRVDAAALSLKLNNAKLGISFNSISAVDNGSLANTPHLR 242
DB 242 KVLPEKIPDVVELYLDGNQFLTV-PKELSNYKHLTLIDLNNRISTLSNOKFSNNTQL 300
QY 243 ELHLDNNKLTFRP-----GGLAHKYIQVYLVHNNNISVSSSDFCPPGHNTKKAISYGS 298
DB 301 TLLLSNRLRCLPPRFDEL---KSLRLSLHGNDSLV-----PEGANLDSLASHLA 351
QY 299 LFSNPV-----QYBLOPSTFRC 316
DB 352 IGANPLYCDQNMQLSDWVKSEYKE--PGIANC 382

RESULT 22
S71876
Fibromodulin - chicken
C:Species: Gallus gallus (chicken)
C:Date: 14-Feb-1997 #sequence revision 13-Mar-1997 #text_change 24-Sep-1999
C:Accession: S71876
R:Nurumakeya, M.V.; Birk, D.E.
Biochem. J. 317, 785-789, 1996
A:Title: Differential expression of fibromodulin mRNA associated with tendon fibril g
A:Reference number: S71876; PMID:96332470; PMID:8760363
A:Accession: S71876
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-380 <NUR>
A:Cross-references: EMBL:U34977; NID:g1098905; PIDN:AAC60016.1; PID:g1098906
C:Superfamily: fibromodulin; leucine-rich alpha-2-glycoprotein repeat homology

Query Match 17.4%; Score 298.5; DB 2; Length 380;
Best Local Similarity 30.1%; Pred. No. 2.4e-14;
Matches 81; Conservative 50; Mismatches 119; Indels 19; Gaps 7;

QY 24 CPFRQCHLRVQCSDLGLDKVPKDLPPDTLLDLONNKITEIKDGFKTLKLNHALIL 80
DB 80 CPQECDCPPNFPNPMYCDNNLTKLP-FVPTRMKYVVFQNNQITLQEGAFNDATLEML 138

```

QY 81 ILVNNKIS--KPSGAFPLVYKLERLYISKQKLEPEKPKTKTQELRAHNEITTKYKV 138
 Db 139 ALHNNOISSEKQKRVFAKLNKRLYNNNNNTKMPSPRLPSRLREHLSTYQKSVPSN 198
 QY 139 TFNGLNQIVIELGTNPILKSSGIENGAFQMKLSYIRIADTNTISTIQGLPSTELHL 198
 Db 199 ALBELNLTALYLSHNTIFEMG---ASLKGKSLILADLSYNHARKVPDGLPMLBOLYL 255
 QY 199 DGNKISRVDASLKGNNLNLATGLSPNSISAVDNGSLA---NTPHLREHLDDNNKLT 254
 Db 256 EYNYINMIPDDYFKVSPPLLYVRMSHSLT---KQGLSTNPNSSSIIELDSTNRLOKI 312
 QY 255 PGGLAEHKYIOVYTLHNHNNISVSSSDFC 283
 Db 313 P--RVSTNENLYIQGQINEFSISSFC 338

RESULT 23

JE0176
 orphan G protein-coupled receptor precursor - human
 C/Species: Homo sapiens (man)
 C/Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 21-Jul-2000
 C/Accession: JE0176
 R/McDonald, T.; Wang, R.; Bailey, W.; Xie, G.; Chen, F.; Caskey, C.T.; Liu, Q.
 Biochem. Biophys. Res. Commun. 247, 266-270, 1998
 A/Title: Identification and cloning of an orphan G protein-coupled receptor of the glyco
 A/Reference number: JE0176; MUID:98308104; PMID:9642114
 A/Accession: JE0176
 A/Molecule type: mRNA
 A/Residues: 1-907 <MCD>
 A/Cross-references: GB:AF062006; NID:93366801; PID:MAC28019.1; PID:93366802
 C/Comment: This protein is a receptor for a novel class of glycoprotein ligands.
 C/Genetics:
 A/Gene: HG38
 A/Map position: 12q22-23
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:562-583/Domain: transmembrane #status predicted <TM1>
 F:594-616/Domain: transmembrane #status predicted <TM2>
 F:639-660/Domain: transmembrane #status predicted <TM3>
 F:661-701/Domain: transmembrane #status predicted <TM4>
 F:725-744/Domain: transmembrane #status predicted <TM5>
 F:768-791/Domain: transmembrane #status predicted <TM6>
 F:803-824/Domain: transmembrane #status predicted <TM7>

Query Match 17.3%; Score 295.5; DB 2; Length 907;
 Best Local Similarity 30.3%; Pred. No. 1.3e-13;

Matches 82; Conservative 50; Mismatches 124; Indels 15; Gaps 6;

QY 24 CFFRCQCH-----LRVQCSDLGIDKVPKDLPPDTLLDQNNKITEIKDGFKNLNLH 78
 Db 34 CPHCHCEPDGRMLLRVDCSDLGISELPSNLSVFTSYLDSMNNISQGLPPLPSLAFLE 93
 QY 79 ALILVNNKISKVSPGATPLVYKLERLYLSKQKLEPEK---PKTQELRAHNEITTKY 135
 Db 94 ELRLAGALTYIPKGAATGYSLSKVLMLQNNQHLHVEALQMLRSIQSLRLDANHISYV 153
 QY 136 RKYTFNGLNQIVIELGTNPILKSSGIENGAFQMKLSYIRIADTNTISTIQGLPSP 192
 Db 154 PSCGSLSHSLRLHMLDDNLTEIPVQ--AFRSLALQMTLALNKIHLIPDYAFGLSS 211
 QY 193 LTELHLDGNKISRVDASLKGNNLNLATGLSPNSISAVDNGSLANTPHLEHLDDNNKT 252
 Db 212 LVVTLHNHNNIHSIGKCCPDGLSHLETLTDANNYLNDEFP--AIRTLNLKELGPHSNIR 270
 QY 253 RVP--GGIAEHKYIOVYTLHNHNNISVSSSDF 282
 Db 271 SIPEKAFVGNPSLITTHFYDNPLOFVGRSAF 301

RESULT 24
 A53860
 chondroadherin precursor - bovine

N/Alternate names: 38k leucine-rich protein
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 05-Nov-1999
 C/Accession: A53860
 R/Name: P.J.; Sommarin, Y.; Boynton, R.E.; Heinegard, D.
 J. Biol. Chem. 269, 21547-21554, 1994
 A/Title: The structure of a 38-kDa leucine-rich protein (chondroadherin) isolated fro
 A/Reference number: A53860; MUID:94342341; PMID:8063792
 A/Accession: A53860
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-361 <NEA>
 A/Cross-references: GB:U08018; NID:9470671; PID:AAA21330.1; PID:9470672
 C/Superfamily: leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan carbox
 C/Keywords: disulfide bond
 F:300-346/Domain: proteoglycan carboxyl-terminal homology <PCH>

Query Match 17.1%; Score 293; DB 2; Length 361;
 Best Local Similarity 27.4%; Pred. No. 5.6e-14;

Matches 92; Conservative 67; Mismatches 129; Indels 48; Gaps 11;

QY 18 PSIGVCPFRQCH--LRVQCSDLGIDKVPKDLPPDTLLDQNNKITEIKDGFKNLX 75
 Db 20 PALA-ACPQCHCHSDQHVYCDKVGQDKIPK-VSEKTKLNTQNNPVLATNSFRAMP 77
 QY 76 NLHLILVNNKISKVSPGATPLVYKLERLYLSKQKLEPEKPKTKTQELR--AHNEI 132
 Db 78 NLVSLHGHQIQRVAVAGARGLKQLYLTLSHNDIVLAGAFDDLTETLYLYLDHNV 137
 QY 133 TKVRKVTENGQIVIELGTNPILKSSGIENGAFQMKLSYIRIADTNTISTIQGL 189
 Db 138 TELPRGLSLPLVNLFIQLNKKIRE--LMSGAFQAGKDLRWLYLSNSSLQPGALDD 195
 QY 190 PPSITELHLDGNKISRVDASLKGNNLNLATGLSPNSISAV--DNGSLANTPHLEHLND 248
 Db 196 VENLAKFYLDNRQSSVPSAALSRLRVEELKLSHNPDKSI PDNAFQSPFRYLETWLDN 255
 QY 249 NKLTRV-PGGLAEHKYIOVYTLHNHNNISVSSSDFCPGNTKASVSGVSLSPNQYW 307
 Db 256 TNLKPSDGAFLVYTLAKVHLNNRLHQLP-----NFPDSLITLTINP---W 304
 QY 308 E-----IOPSTRCVYVR 320
 Db 305 KTCQLRLRLRLWLEAKTSRDPATCASPAKRGQHHR 340

RESULT 25

A58532

glial cell membrane glycoprotein LIG-1 precursor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 05-Nov-1999
 C/Accession: A58532

R/Suzuki, Y.; Sato, N.; Tohyama, M.; Wanaoka, A.; Takagi, T.
 J. Biol. Chem. 271, 22522-22527, 1996
 A/Title: cDNA cloning of a novel membrane glycoprotein that is expressed specifically
 A/Reference number: A58532; MUID:96394313; PMID:8798419
 A/Accession: A58532

A/Status: preliminary; translated from GB/EMBL/DBS
 A/Molecule type: mRNA
 A/Residues: 1-1091 <SUZ>

A/Cross-references: GB:D78572; NID:91545806; PID:BA11416.1; PID:91545807
 F:36-61/Domain: proteoglycan amino-terminal homology <PAH>
 F:71-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F:95-117/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:118-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F:142-165/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
 F:166-189/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
 F:191-213/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
 F:214-237/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
 F:238-261/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
 F:262-285/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
 F:286-309/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>

F:310-333/Domain: leucine-rich alpha-2-glycoprotein repeat homology <RR1>
F:334-357/Domain: leucine-rich alpha-2-glycoprotein repeat homology <RR2>
F:358-381/Domain: leucine-rich alpha-2-glycoprotein repeat homology <RR3>
F:383-408/Domain: leucine-rich alpha-2-glycoprotein repeat homology <RR4>
F:409-432/Domain: leucine-rich alpha-2-glycoprotein repeat homology <RR5>
F:440-485/Domain: proteoglycan carboxyl-terminal homology <RCH>

Query Match	17.0%;	Score 291;	DB 2;	Length 1091;
Best Local Similarity	30.7%;	Pred. No. 3.6e-13;		
Matches	84;	Conservative	121;	Indels 14; Gaps 8;

QY 24 CPEFCOCHLRVVOCSDDLGRKVEKDIPEPDITLLDLONNKITEIKOGDFNKILKNITLIV 83

Db 43 CAACTCAGNSLDSCSGGLATLPDRLPSWTRSLNLSYNLSLSDBAFEDTLNLOEYVLN 102

QY 84 NNKLSKVSPEGAFPLVVLGERLRYLSKQOLKELPEKMK--TLQELRAHENEITTKRKYTF 140

Db 103 SNELTAL-PSLGTASLIVVSLFLQHNKLSLVDSQKLSYLSLEVLDSLNNITTEIRSCF 161

QY 141 -NGANQIVIELGTNPFLKSGIENGAFQGM-KLGYIRADINITSIGGL-PSLTEL 194

Db 162 PNGIR---IRELNINLSRISLILSGAFDGLSRSLTLTRLSKRITQLPVPKAFKRLRLQL 211

QY 197 HLDGNKISRVDASLKGANNIAKGLSFSNISAVDNGSLANTPHLREHLDDNNKILTRY-P 255

Db 219 DLANNRIRLIEGLTFQGLDSLLEVTLRLORNNISRLTGDGAFWGLSKKHVLLEYNLSVEVNS 276

QY 256 GGLAEHKYIQVYVYLNHNNSIVGSS--DPEPPCH 287

Db 279 GSLYGLTALHQLHLNNSISIRIQDQMSFCQKILH 312

RESULT 26

G protein-coupled receptor FEX - mouse
 C.Species: Mus musculus (house mouse)
 C.Date: 23-Jul-1999 #sequence-revision 23-Jul-1999 #text-change 11-May-2000
 C.Accession: JG0193
 R.Hermey, G.; Methner, A.; Schaller, H.C.; Hermans-Borgmeyer, I.
 Biochem. Biophys. Res. Commun. 1994, 273-279, 1999
 A.Title: Identification of a novel seven-transmembrane receptor with homology to glycoprotein
 A.Reference number: JG0193; PMID:99121227; PMID:9920770

Query Match	16.7%	Score 285.5	DB 2	Length 907
Best Local Similarity	30.5%	Pred: No. 7e-13		
Matches	84	Conservative	50	Mismatches 118; Indels 23; Gaps 8

QY	24	CFPRCQCHU--RV---VOCSDGLDVPDQPPDPTLIDLONNKXTIEKDGDFOKUKLKH	78
Db	34	CFSHCHCELDGMLRLVDCSDJGSLSEPNLSVFPISYIDLMSNNISQGLASLHLRCFIE	93
QY	79	ALIIVNNKISKVSPGAFPTPLVKLEIRLYSKNOJKEJPEKM---PKTLQELRAHEKITVY	135
Db	94	EIRLGNALMTHTPKGAFTGTLHSLKTVLMONNOILRKVEEBALONTLSLOSLRDANHSYV	153
QY	136	RKVTPNGLNQMIVIEHGTNPGLKSSGGENAPQGMKLSYIRADNTNITSIPQ--GLPPS	192
Db	154	PSCSCSGHLSLHMLMDNALTDVPQO--AFPSLSLQAMTALINKIHHIIDLAYAFENISS	211
QY	193	LTELMDGNKISRVDAAISLKGILNTAKGLSPFISISAVNGSIANTPHILREILNNKLT	252
Db	212	LAVLHLNNRHISLGKCFDGLHSLFETLADLNNNLDEPPT-AIKTSLNKELGFSNNIR	270
QY	253	KVPGGLAEHKYIQ-----VVIYLANNTISVSGSDF	282
Db	271	SIP---ERAFVGNBSLITITHFVDNIQVGVSAF	301

RESULT 27

neumoral leucine-rich repeat protein-3 - rat
JC67763
Cispecter: Rattus norvegicus (Norway rat)
Feb 2003 About 3000 bp

A:Title: Rat neuronal leucine-rich repeat protein-3: Cloning and regulation of the gene
A:Reference number: JC7763; PMID:11549284
A:Contents: Fibrosarcoma cells
A:Accession: JC7763
A:Molecule type: mRNA
A:Residues: 1-707 <PDB>
A:Cross-references: GB:AF291437
C:Comment: This protein, a new member of the neuronal leucine-rich repeat protein family in protein-protein interaction and functions as a cell adhesion molecule or soluble 1
C:Genetics:
A:Gene: nltr-3.
C:Keywords: cell adhesion

Query Match 16.5%; Score 283.5; DB 2; Length 707;
Best Local Similarity 28.4%; Pred. No. 6.9e-13;
Matches 99; Conservative 52; Mismatches 126; Indels 71; Gaps 13;

[illegible]

RESULT 28

Insulin-like growth factor acid-labile chain - baboon
C:Species: Papio sp. (baboon)
C:Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
C:Accession: J05239
R:Delahanty, P.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 227, 897-902, 1996
A:Title: The cloning and expression of the baboon acid-labile subunit of the insulin-
A:Reference number: J05239; MUID:97040714; PMID:8886027

Query Match	15.9%	Score 273;	DB 2;	length 605;
Best Local Similarity	25.9%	Pred. No. 3.3e-12;		
Matches 87; Conservative	58;	Mismatches 139;	Indels 52;	Gaps 9;

```

QY      5 GIGPEVDDDRDEPRLGVPVCPFRQC-----HLRVQCSDLGLDKVPKDLPPDTLLDL 58
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
          : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      27 GAPEPTGEAL-----GPACPRATCACSYDDEVNELSVFCSSRNLTRLPDGIPGGTQALWL 81

```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2004, 09:36:44 ; Search time 84 Seconds
(without alignments)
1010.706 Million cell updates/sec

Title: US-10-004-176-6

Sequence: 1 VASAGIGPEVPDRDPFPEPL.....QPTFCVYVRSAGIOLGVNK 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvtnus:*
16: sp_bacteriapi:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1229	71.7	359	13 Q9DE03	Q9de03 oreochromis
2	895.5	52.3	410	13 Q9DD27	Q9dd27 petromyzon
3	894.5	52.2	310	13 Q9DD28	Q9dd28 petromyzon
4	887.5	51.8	347	13 Q9DE00	Q9de00 petromyzon
5	883.5	51.6	370	13 Q9DE04	Q9de04 oreochromis
6	878.5	51.3	388	13 Q9DD29	Q9dd29 petromyzon
7	817.5	47.7	325	4 Q8NAB7	Q8nab7 homo sapien
8	784	45.8	224	13 Q9DE01	Q9de01 brachydanio
9	548.5	32.0	187	4 Q9NXP3	Q9nxp3 homo sapien
10	487	28.4	96	11 Q63156	Q63156 rattus norv
11	385.5	22.5	378	11 Q8CAZ9	Q8caz9 mus musculu
12	342	20.0	627	4 Q8NC95	Q8nc95 homo sapien
13	341	19.9	649	11 Q8BGT1	Q8bgt1 mus musculu
14	334.5	19.5	1534	4 Q75093	Q75093 homo sapien
15	334.5	19.5	1618	4 Q9UTI7	Q9uti7 homo sapien
16	332	19.4	674	4 Q8WVA2	Q8wva2 homo sapien

17	330	19.3	120	13 Q9DE02	Q9de02 brachydanio
18	328.5	19.2	1531	11 Q9WV55	Q9wv55 mus musculu
19	328	19.1	1523	11 Q9WV44	Q9wv44 mus musculu
20	327.5	19.1	1531	11 Q88279	Q88279 rattus norv
21	327	19.1	1523	11 Q88280	Q88280 rattus norv
22	325	19.0	1440	5 Q20204	Q20204 caenorhabdi
23	325	19.0	1512	13 Q9DE36	Q9de36 brachydanio
24	324.5	19.0	1523	4 Q75094	Q75094 homo sapien
25	324.5	18.9	1474	11 Q8CUG9	Q8cug9 rattus norv
26	323.5	18.9	1458	11 Q8CUG8	Q8cug8 rattus norv
27	322	18.8	1529	4 Q94813	Q94813 homo sapien
28	321.5	18.8	376	4 Q8IV47	Q8iv47 homo sapien
29	318.5	18.6	1515	13 Q9DE37	Q9de37 brachydanio
30	318	18.6	1521	11 Q9R1B9	Q9r1b9 mus musculu
31	317	18.5	1525	4 Q9Y507	Q9y507 homo sapien
32	316.5	18.5	1530	11 Q9WU55	Q9wu55 rattus norv
33	316	18.4	1530	13 Q9WU23	Q9wu23 xenopus lae
34	315	18.4	1521	4 Q95710	Q95710 homo sapien
35	314	18.3	1095	13 Q9XG44	Q9xg44 mus musculu
36	313	18.3	1095	13 Q9XG44	Q9xg44 gallus gall
37	312.5	18.2	798	4 Q8WV22	Q8wv22 homo sapien
38	309.5	18.1	796	11 Q8BNJ3	Q8bnj3 mus musculu
39	309.5	18.1	796	11 Q8WV21	Q8wv21 rattus norv
40	307.5	18.0	1346	5 Q9V477	Q9v477 dirosophila
41	307	17.9	396	11 Q8C3D9	Q8c3d9 mus musculu
42	303.5	17.7	652	11 Q9PPI1	Q9ppi1 mus musculu
43	303.5	17.7	653	4 Q9HBM1	Q9hbm1 homo sapien
44	302.5	17.7	406	11 Q8CJH0	Q8cjh0 rattus norv
45	302	17.6	640	4 Q9HCJ2	Q9hcj2 homo sapien

ALIGNMENTS

RESULT 1

Q9DE03 PRELIMINARY; PRT; 359 AA.
AC Q9DE03;
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DE Decortin.
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acantopterygia; Acantopterygii; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20496956; PubMed=11040287;
RA Shintani S., Sato A., Toyosawa S., O'hugin C., Klein J.,
RT "Biglycan-like extracellular matrix genes of agnathans and teleosts.",
J. Mol. Evol. 51:363-373(2000).
DR EMBL; AF247822; AAG40157.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003581; LRR_Typ.
DR Pfam; PF00560; LRR_7.
DR Pfam; PF01462; LRRNT_1.
DR SMART; SM00013; LRRNT_1.
DR SMART; SM00369; LRR_Typ_1.
DR PROSITE; PSS0506; LRR_TYP; 2.
SQ SEQUENCE 359 AA; 39807 MW; F19F9AA4E7572C6 CRC64;

Query Match

Best local similarity 71.7%; Score 1229; DB 13; Length 359;
Matches 229; Conservativity 46; Mismatches 53; Indels 2; Gaps 2;

QY 1 VASAGIGPEVPDRDPFPEPL-GVPCPRQCCHLRVQCSDLGLDKVPRHDLPTDTLLDQ 59
DB 29 WEDESGGPEVTS-PLPVTGSGKPCFRCOCHLRVQCSDLGLKAVPBDIPDPTLLDQ 87

Qy	60	NNKITTELKODPFNLKNTLHALLIANNKSKVSPGAFTEVLVYLERLYLSKQKTELPERMP	112
	88	NNKITTELKENDFNLGLHALLIANNKLTITTHPKAFSPULYKLORYLISKLLKEMPMNP	147
Qy	120	KTLQELRAHENEITKYRKYVTFENGLNOMVIELGTNPXSGIENGAFQGMKQLSYIRIAD	179
Db	148	KSIOELRIHENEITTKKKASFOGMSHVIYMEIGSNPLTKAGIEAGAFADLKRASYIRIAD	207
Qy	180	TNITSIPQGLPELITELHLDGKIKSHVDAASLKGIANNAKIGLSPNGLSAANDNSLANTP	239
Db	208	TNITEVPKGPSSLSELHLDGKNKITLTLADRIKGMKNLAKIGLSYNOJLSVENETLSNAP	267
Qy	240	HLRELHLDNKKLTRVPGGLAEHKYLOVVYLANNNNISVYSGSDPFCPBGHNTKKASYSQVL	299
Db	268	HLRELHLDNNAALTSVPPGLPDHKYILOVVYLAHAKIAAVOTDEFCPBGNTKKANYSQVL	327
Qy	300	FSNPVQYMELOPSTFPCYVRSALIOGANK	329
Db	328	FSNVEPYMEVOPVTFRCVDFRSALIOGANK	357

Query Match	52.3%	Score 895.5	DB 13	Length 410
Best Local Similarity	53.6%	Pred. No. 2,4e-54		
Matches 173	Conservative 51	Mismatches 90	Indels 9	Gaps 2
QY	8	PEVPPDRDPEBSELGVCPCPCQCHLRVQCSTLGDRTPKDLPETTLIDIDONNKITEIK	67	
DB	95	PPPPPDAS-----CPFGCCCSARVQCSPLGVSVPQALPKDARLIDIDONNKITEIK	146	
QY	68	DODFNLKNLIALILVNKKISVSGAFPLVTKERIVLSKNQLELPEKKPKTQLQELRA	127	
DB	147	ODDFGLKNTALVYLVNMLISKVBPAPAPLSSLDKLYISHQLTREVPQSWSSLVELR	206	
QY	128	HENETTKRVKVFENGLNQWIVLELTNPILSSGSEINGAFQCGKKLSTYRIADNTITSIPQ	187	
DB	207	HENNIKIKPKAFSGMKRKLHLEMGKNPLQSGIIVGAFEGEGLRVLVYRVSDSKLARLPK	266	
QY	188	GIPESLTEILHLDGNKISRVAASLKLGNLNAKLGSFNSISAVDNGSLANTPHIREHLD	247	
DB	267	DLPSNIOEILHEHNDITALEQEDLIRYPLRIHRLGHSYNDIKIVQNGSLJETCPHIREHLD	326	
QY	248	NNKLTIRVREGLAHEKTIQVYVYLAHNNNISVSGSDPCPCGHNTKASYSGVSLFSNPQVYW	307	
DB	327	SNVLTVQVPEGALFLKHLQVYVYLAHNSKRLAIVKSDDFCSKASPKRLVYSGISLFDNPVYW	386	

QY 308 EIQPSTFRCVVRSALQLG-NYK 3229
::||| |::
Db 387 DVPSAIFRCVASRSAVQFSQNFR 4099

RESULT 3	Q9DDZ8	PRELIMINARY;	PRT;	310 AA.
ID	Q9DDZ8			
AC	Q9DDZ8;			
DT	01-MAR-2001 (TrEMBLrel. 16, Created)			
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)			
DE	Biglycan-like protein 2 (Fragment).			
GN	BGL2.			
OS	Petromyzon marinus (Sea lamprey).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;			
OC	Petromyzontiformes; Petromyzontidae; Petromyzon.			
OX	NCBI_TaxID=7757;			
LN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEBLINE=20436956; PubMed=11040287;			
RA	Shintani S., Sato A., Toyosawa S., O'higin C., Klein J.;			
RT	"Biglycan-like extracellular matrix genes of agnathans and teleosts.";			
RL	J. Mol. Evol. 51:363-373(2000).			
DR	EMBL; AF247827; AAC40162.1; -.			
DR	InterPro; IPR001611; LRR.			
DR	InterPro; IPR000372; LRR_Nterm.			
DR	InterPro; IPR003591; LRR_Typ.			
DR	Pfam; PF00560; LRR_7.			
DR	Pfam; PF01462; LRRNT_1.			
DR	SMART; SM00013; LRRNT_1.			
DR	PROSITE; PSS0506; LRR_TYPICAL; 2.			
FT	NON_TER			
SE	SEQUENCE 310 AA; 34572 MW; 6FB8E05B14339EF5 CRC64;			

Query Match	52.2%	Score 894.5	DB 13	Length 310
Best Local Similarity	55.4%	Pred. No. 1.9e-54		
Match 170	Conservative 51	Mismatches 85	Indels 1	Gaps 1
Qy	24	CPFRCCGHLRVVCGSDLGIDKVPDLPDDTLLDLONNKTEIKDGFKNLKNLHALLV	83	
Db	3	CPFGCCGSAARVVCSDLGIVSPQAIKRDARLLDLONNKTEIKQDDFKGLNLYLV	62	
Qy	84	NNKISKVSPGAFPLVYKLEIRLYLSKNQLELPEKPKPTLOELRAHENEITVRKVTENG	143	
Db	63	NNLSKVPKPAFAPLSSLDKLYISHNQTEVPGSMPSLVELRHENNIKKIPDAFGSM	122	
Qy	144	NQMTVIELGNTPKLSGIEGAPGQMKLSTIRADNTNITSIPQGLPPLSTELHLDGKI	203	
Db	123	KRLHAEWGGNPLDOSTGIEVGAPEGLERLVYVRSDSKLARIPDLPSPIDELHLEHQI	182	
Qy	204	SRVDAASLKGALNLAKLGISFNSSISAVDNGSLANTPHRLHLNNKLTTRVPGGLAERKY	263	
Db	183	TALQEDILIRYPLHRLGLSTNQIKVIONGSLFCPHRLHLSDSNVLTQVPGGLAFKX	242	
Qy	264	IQVVYLIHNNNISVVGSSDFCPGHNATKASVGSLSNPQVMEIOPSTRCCVYVSRAI	323	
Db	243	LQVYLIHNNKLAAYKSDDFCSKASPKRYVLSGISLPNVMYMDVPSARFCAVSRAV	302	
Qy	324	QLG-NYK 329		
Db	303	QFSQWFR 309		
RESULT 4				
Q9DE00				
AC Q9DE00	PRELIMINARY	PRT	347 AA	
DT 01-MAR-2001	(Tremblrel. 16	Created)		
DT 01-MAR-2001	(Tremblrel. 16	Last sequence update)		
DT 01-MAR-2003	(Tremblrel. 23	Last annotation update)		
DE	Biglycan-like protein 1 (Fragment)			

GN	BLG1.
OS	Petromyzon marinus (Sea lamprey).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC	Petromyzontiformes; Petromyzontidae; Petromyzon.
OK	NCBI_taxid=7757;
RN	(1)
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20496956; PubMed=11040287;
RA	Shantani S., Sato A., Toyosawa S., O'huiglin C., Klein J.;
RT	"Biglycan-like extracellular matrix genes of agnathans and teleosts.,"
RL	J Mol Evol 51:336-372(2000).
DR	EMBL, AF247825; AAC60160.1; --
DR	InterPro, IPR001611; LRR.
DR	InterPro, IPR003572; LRR_Nterm.
DR	InterPro, IPR003591; LRR_typ.
DR	Pfam; PF00560; LRR; 8.
DR	Pfam; PF01462; LRRNT; 1.
DR	SMART; SM00013; LRRNT; 1.
DR	PROSITE, PSS0506; LRR_TYPICAL; 1.
FT	NON_TER
Q-	SEQUENCE 347 AA; 38266 MW; 55CC296938CED391 CRC64;

Query Match	51.8%	Score	887.5	DB	13	Length	347
Best Local Similarity	54.4%	Pred.	NC.6.9e-54				
Matches	178	Conservative	50	Mismatches	90	Indels	9
						Gaps	3

QY	4	SGIGPEVDDDDFPEPSLGPVCEPFRQCHILRVQCSDDLGLDKVPKOLPPDTLLDLQNNKI	63
DB	28	SPVAPPGQ-----PSVG--CPFGQGSRLRVQGSDDLGLKSPASIPDABAVNDLQNSKI	79
QY	64	TEIKDGPDKNLKLNHALLLVNNKSKSVBPAAFTPLVLTLELYLSXQQLKEPEKPKTLQ	123
DB	80	TEIKDQDDPKGLOALHALPLVNNLLIAKIPKAPAPVAVSDKUYISHNRLEVPFGTGPISLI	139
QY	124	ELRAHENEITVRYKTYTFENGLOMITYELGTNPDLKSSGJENGAFOQMKLSYLRIMDIT	183
DB	140	ELRAHENEIKRYPKOTFINNGQLHYLEIGKNPLPSSGJLEVGAENGLDKTYLRISYSKLT	199
QY	184	SIPOGLPESLTEIHDGDKNKISRVDAASLKGILNNLAKLGIFNSISAVDNGSLANTPHARE	243
DB	200	QLPEKELPMSLEHMEGMEIYALIEBDELFGIYLRDLGSLSTYKITEVQNGSLAVSGNLPRE	259
QY	244	LHLDNNKLTTRVPGGLAEHKYIQVYVYLLANNNISVWGSSDFCEPBGHNTTKAASYSVGLFSNP	303
DB	260	LHLDNNLLVSVYPGSKLRSNLVYVYLLHNSKIKEYVPTDCCPFWSPKQAQVYGISLYDNP	319
QY	304	VOYMEIQOSTRCVTVRSALQLG-NYK 329	
DB	320	VYMEVPPSVPRCVNHNNAIHFGSNYR 346	

RESULT 5			
ID	Q9DE04	PRELIMINARY;	PRT; 370 AA.
AC	Q9DE04;		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)		
DE	Biglycan-like protein 3.		
GN	Bgl3.		
OS	Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
OC	Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidae;		
CC	Chilidae; Oreochromis.		
OX	NCBI_TaxID=8128;		
NP	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20496956; Pubmed=11040287;		
RA	Shintani S., Sato A., Toyosawa S., O'Nigin C., Klein J.;		
RT	"Biglycan-like extracellular matrix genes of agnathans and teleosts.";		
RL	J. Mol. Evol. 51:366-373(2000) .		
DR	EMBL; AF247821; AAG40156.1; -		

DR InterPro: IPR001611; LRR.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR003591; LRR_typ.
DR Pfam: PF00560; LRR; 9.
DR Pfam: PF01462; LRRNT; 1.
DR SMART: SMO0013; LRRNT; 1.
DR PROSITE: PSS0506; LRR_TYPICAL; 2.
SQ SEQUENCE 370 AA; 42177 MW; BCD0675694ECA287 CRC64;

Query Match	51.6%	Score 883.5	DB 13	Length 370
Best Local Similarity	53.0%	Prod. No. 1.4e-53		
Matches 170	Conservative 53	Mismatches 97	Indels 1	Gaps 1
Qy	9	EVPPDRDPEPSLGFVCEPCRCOCHLRVVCOSDLGLDKVPKDLPEPTLLDLONNKITEIKD	68	
Db	50	EVDDDDDDDDVDEBDCGPAHCHGCSRRVVCSDQGLISVPDKIPEDTWIMDLQNNIDITELIQ	109	
Qy	69	GDFPNLKNLHALIIVNNKISKVSPGAFITPLVCLERLYLSKNQKELPEKKMPKITQELRAH	128	
Db	110	DDFPGKMLKLYGLFLINNKISRIRHPKAKKMNDRILTLSTYMLNEIPANLPVNYIELRPH	169	
Qy	129	ENETTKRYKATFENGLOMIYIELGTNTKNSGTEENGAFQMKULSYIRADINTSLPQG	188	
Db	170	ENQIDRLOKQAFKRLCHVLEIGANPLTNSGLEIGAFNGLSTL-YIGIAAKULTSLPKD	228	
Qy	189	LPEPSITELHLDGNKISRVDAASLTGLANLAKGLSPFASISAVDNGSLANPPLHLEHLDN	248	
Db	229	FPSSITTELSLDYNNKISKEVEIEDFRKNLOLQRLGALFAPQIKYVENGSLANPPLKIREIYLDN	288	
Qy	249	NKLTRVPGGLAEHKYITDVVYLIHNNNISVAGSSDFCPGHNTKKASYSYGVSLSFSPVOYWE	308	
Db	289	NRMKAVPFGSLSLTYLQVITFLAHGKNTSISVGINDFCPIRADSKNPNYGISLIFANPVKXWA	348	
Qy	309	IQPSFRCVYVRSALQIGNYK	329	
Db	349	IQPATERCVYGRRGVQLGNFR	369	

RESULT 6			
ID	Q9DDZ9	PRELIMINARY;	PRT; 388 AA.
AC	Q9DDZ9;		
DT	01-MAR-2001 (TREMBLrel.16, Created)		
DT	01-MAR-2001 (TREMBLrel.16, Last sequence update)		
DE	01-MAR-2003 (TREMBLrel.23, Last annotation update)		
DR	Biglycan-like protein 1 (Fragment).		
GN	BGL1.		
OS	Petromyzon marinus (Sea lamprey).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;		
OC	Petromyzontiformes; Petromyzontidae; Petromyzon.		
OX	NCBI_TaxID=7757;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEBLINB=20496956; PubMed=11040287;		
RA	Shintani S., Sato A., Toyosawa S., O'huiginn C., Klein J.;		
RT	"Biglycan-like extracellular matrix genes of agnathans and teleosts.";		
RL	J. Mol. Evol. 51:363-373(2000).		
DR	EMBL; AF247826; AAC04161.1; -.		
DR	InterPro; IPR001611; LRR.		
DR	InterPro; IPR000372; LRR_Nterm.		
DR	InterPro; IPR003591; LRR_Cyp.		
DR	Pfam; PF00560; LRR; 8.		
DR	Pfam; PF01462; LRRNT; 1.		
DR	SMART; SMO0013; LRRNT; 1.		
DR	PROSITE; PSS0506; LRR_TYPICAL; 1.		
FT	NON TER 1		
SQ	SEQUENCE 388 AA; 42542 MW; 2507169E9BB6071B CRC64;		

Query Match 51.3%, Score 878.5; DB 13, Length 386;
Best Local Similarity 53.8%, Pred. No. 3,4e-53;
Matches 176; Conservative 52; Mismatches 90; Indels 9; Gaps 3;


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Db      69  SEVADPOF-----PSVG--CFGGCCSIRVVOCSDLGLKSVAPAGIPKARAVMDLQSNKI 120
Qy      64  TEIKQDGFNLKNTLHLLVNNKISKVSBCAFTPLVKERLYLSKQKLEPERKPKTQ 123
Db      121  TEIKQDGFNLKNTLHLLVNNKISKVSBCAFTPLVKERLYLSKQKLEPERKPKTQ 180
Qy      124  ELRAHENEITTKYKRVTFNGNLQMIIVLELGTNPLKSSGIEGNGAFQGGKLSYRIADTNT 183
Db      181  ELRAHENEITTKYKRVTFNGNLQMIIVLELGTNPLKSSGIEGNGAFQGGKLSYRIADTNT 240
Qy      184  STPQGLPSGLTEHLHDGKNTISRVDAASLKLNNLAKLGSFNSISAVNGSLANTPHLRE 243
Db      241  QLPKELPNSILTEHLHLEGNIEVAIEDEDLFGYPYLFELGLISYKNTIEVQNGSLAVSGNLE 300
Qy      244  LHLNNKLTFRVPGLAEHKTIQVYVLIHNNNISVSGSDPCPGHNTKKASYSGVSLFSP 303
Db      301  LHLNNKLTFRVPGLAEHKTIQVYVLIHNNNISVSGSDPCPGHNTKKASYSGVSLFSP 360
Qy      304  VQYWEIOPSTFRVCYVRSALQGL-NYK 329
Db      361  VQYWEIOPSTFRVCYVRSALQGL-NYK 387

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RESULT 7

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QSNAB7  ID 08NAB7 PRELIMINARY; PRT; 325 AA.
AC 08NAB7;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypochemical protein FLJ35635.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Hoshino T., Kanehori K., Yoshida M., Watanabe S., Ishida S., Ono Y.,
RA Hoshino T., Kanehori K., Yoshida M., Watanabe S., Ishida S., Ono Y.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A.,
RA Ishii S., Yamamoto J., Isono Y., Kawai-Hiro Y., Saito K., Nishikawa T.,
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Magatsuma M., Takahashi-Fuji A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Negahara K., Maehuo Y., Nagai K., Isogai T.;
RT "NEO human cDNA sequencing project."
RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK092954; BAC04007.1; -.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR003591; LRR_cyp.
DR Pfam; PF01462; LRRNT_1.
DR SMART; SM00013; LRRNT_1.
DR PROSITE; PS50506; LRR_TYPICAL; 2.
KW Hypochemical protein.
SQ
SEQUENCE 325 AA; 3637 MW; 33BAC7DEB17982BE CRC64;

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Query Match 47.7%; Score 817.5; DB 4; Length 325;
Best Local Similarity 49.8%; Pred. No. 4,6e-49;
Matches 164; Conservative 40; Mismatches 80; Indels 45; Gaps 3;
Qy 2 EASGIGPE-VPPDRDPEPSLGPVPCRCOCHLRVVOCSDLGLDKVPKDLPPPTLLDLCN 60
Db 40 EASGADTSGVLDPSVTPYTSAMCPGCHLRVVOCSDLGLSKVPEKISPTLLDLCN 98
Qy 61 NKITEIKDGFNLKNTLHLLVNNKISKVSBCAFTPLVKERLYLSKQKLEPERKPK 120
Db 99 -----KLVSKNHLVLEIPNPLS 116
Qy 121 TLQELRAHENEITTKYKRVTFNGNLQMIIVLELGTNPLKSSGIEGNGAFQGGKLSYRIADT 180
Db 117 SLVEIRIHNDRIKRVKGVFSGLRNNNCIEMGNGPLENGFEPGAFDGH-KINYIRISBA 175

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Qy 181 NITSIPQGLPSGLTEHLHDGKNTISRVDAASLKLNNLAKLGSFNSISAVNGSLANTPH 240
Db 176 KLTGIPKDLPTLNLHLDNNKIQALIEDLIRYSKTLRLGIGNQIRKTIENGSLFPT 235
Qy 241 LRELHLDNNKLTFRVPGLAEHKTIQVYVLIHNNNISVSGSDPCPGHNTKKASYSGVSLF 300
Db 226 LRELHLDNNKLTFRVPGLAEHKTIQVYVLIHNNNISVSGSDPCPGHNTKKASYSGVSLF 295
Qy 301 SNPVQYWEIOPSTFRVCYVRSALQGL-NYK 329
Db 296 NNPVQYWEIOPSTFRVCYVRSALQGL-NYK 324

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RESULT 8

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QSNAB7  ID 09DE01 PRELIMINARY; PRT; 224 AA.
AC 09DE01;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Decorin (Fragment).
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN 11
RP SEQUENCE FROM N.A.
RC MEDLINE=20496956; PubMed=11040287;
RA Shintani S., Sato A., Toyosawa S., O'hugin C., Klein J.;
RT "Biglycan-like extracellular matrix genes of agnathans and teleosts."
RT J. Mol. Evol. 51:363-373 (2000).
DR EMBL; AF247824; AAG40159.1; -.
DR ZFIN; ZDB-GENE-010102-1; dcm.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003591; LRR_cyp.
DR Pfam; PF00560; LRR_7.
DR SMART; SM00369; LRR_TYP_1.
DR PROSITE; PS50506; LRR_TYPICAL; 2.
FT NON TER 1
FT NON TER 1
SQ
SEQUENCE 224 AA; 2442 MW; 54A1B7AB9167DF0 CRC64;

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Query Match 45.8%; Score 784; DB 13; Length 224;
Best Local Similarity 68.9%; Pred. No. 6,1e-47;
Matches 153; Conservative 30; Mismatches 39; Indels 0; Gaps 0;
Qy 45 VPKDLPPPTLLDLCNNKITEIKQDGFNLKNTLHLLVNNKISKVSBCAFTPLVKERL 104
Db 3 VPEKIPDPTLLDLCNNKITEIKQDGFNLKNTLHLLVNNKISKVSBCAFTPLVKERL 62
Qy 105 YLSKQKLEPERKPKTQELRAHENEITTKYKRVTFNGNLQMIIVLELGTNPLKSSGIEG 164
Db 63 YLSKQKLEPERKPKTQELRAHENEITTKYKRVTFNGNLQMIIVLELGTNPLKSSGIEG 122
Qy 165 AFQGGKLSYRIADTNTITSIPQGLPSGLTEHLHDGKNTISRVDAASLKLNNLAKLGSF 224
Db 123 AFADLRKVSARIRADTNTITSIPQGLPSGLTEHLHDGKNTITKVTADSLKGLSKLGLSH 182
Qy 225 NSISAVNGSLANTPHLREHLHDGKNTISRVDAASLKLNNLAKLGSF 266
Db 183 NSISAVNGSLANTPHLREHLHDGKNTISRVDAASLKLNNLAKLGSF 224

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RESULT 9

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QSNAB7  ID 09NXP3 PRELIMINARY; PRT; 187 AA.
AC 09NXP3;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)

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DE Hypothetical protein FLJ20129.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Oca T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
 RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK000136; BAA0967.1; -
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR003591; LRR_TYP.
 DR Pfam; PF00560; LRR_3.
 DR PROSITE; PS50506; LRR_TYPICAL; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 187 AA; 21074 MW; BDBEE37373CA3DBE CRC64;

Query Match 32.0%; Score 548.5; DB 4; Length 187;
 Best Local Similarity 53.2%; Pred. No. 1.1e-30;
 Matches 99; Conservative 42; Mismatches 44; Indels 1; Gaps 1;

QY 143 LNMVIELGTNPILKSSGIENGAFQGMKKLSYIRADNTITSIPOGLPSSLTEHLHDGKX 202
 DB 1 MNAHLVLEKSNAPLNDNNGIEPQAFEGV-TVFHRIAEAKLISVPGKLPETLEHLHDGKX 59
 QY 203 ISRVDAASIKGLNNTAKLGLSFNSISAVDNGSLANTPHLRELHNNKLTTRVPGGLAEHK 262
 DB 60 ISTVELDEPKRYKELQRLGLGNKKITDLENGSLANIPRYEHLNENKTKKIPSGLPK 119
 QY 263 YIQVYIHHNNISVVGSSDFCPGKATKASISGSLSENPQYMEIQSTRCYVNSA 322
 DB 120 YIQIIFLHNSIARVAVDPTVPKMKSLYSALSFNNPKYEMOPATERCVLSRMS 179
 QY 323 IQLNNY 328
 DB 180 VOLGNP 185

RESULT 10

063156 PRELIMINARY; PRT; 96 AA.

AC 063156; 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Decorin (Fragment).
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Lung;
 RA Moates-Staats B.M., Stiles A.D., Xu L.;
 RT "Expression of decorin RNA in rat lung undergoing chronic lung
 injury."
 RT Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; L75825; AAA85371.1; -
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR003591; LRR_TYP.
 DR Pfam; PF00560; LRR_3.
 DR PROSITE; PS50506; LRR_TYPICAL; 1.
 FT NON_TER 1
 FT NON_TER 96
 SQ SEQUENCE 96 AA; 10398 MW; C6D19F1750B050D0 CRC64;

Query Match 28.4%; Score 487; DB 11; Length 96;
 Best Local Similarity 100.0%; Pred. No. 9e-27;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 YIRADNTITSIPOGLPSSLTEHLHDGKISRVDASIKGLNNTAKLGLSFNSISAVDNG 233
 DB 1 YIRADNTITSIPOGLPSSLTEHLHDGKISRVDASIKGLNNTAKLGLSFNSISAVDNG 60
 QY 234 SLANTPHLRELHNNKLTTRVPGGLAEHKYIQVYTL 269
 DB 61 SLANTPHLRELHNNKLTTRVPGGLAEHKYIQVYTL 96

RESULT 11

08CA29 PRELIMINARY; PRT; 378 AA.

AC 08CA29; 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Proline arginine-rich end leucine-rich repeat.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 DR EMBL; AK037150; BAC29722.1; -
 SQ SEQUENCE 378 AA; 43293 MW; 6F85A1B935FFB8C CRC64;

Query Match 22.5%; Score 385.5; DB 11; Length 378;
 Best Local Similarity 32.2%; Pred. No. 6e-19;
 Matches 93; Conservative 57; Mismatches 124; Indels 15; Gaps 6;

QY 2 EASGIGPEVPPDRPSPSLGVPCCPC--HLRVQCSLDGLDKVKDLPDPTLLDL 58
 DB 50 EPTDLPPLPPG--PSPVFPDCEPCPCPPDFPSALCDSRNLRVVP-IPRTHLYTL 105
 QY 59 QNNKITEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLELYSKNOLKELPEKM 118
 DB 106 QNNFTTEPLPSFQATGLRVAVLNDNKRIRKVDQVGLKLSLATLNEKQLEVPBAL 165
 QY 119 PRTLOELRAHNEITKRVKTFNGIOMIVIELGTNPILKSSGIENGAFQGMKKLSYIRIA 178
 DB 166 PRNLEQLLSQNLISRIIPGVFSKLENDLLDQHNRLSDGVFKADTFQGLKNLQNLIA 225
 QY 179 DTNITSIFQGLPSSLTEHLHDGKISRVDASIKGLNNTAKLGLSFNSISAVDNGSLANT 238
 DB 226 HNIILKMPKPKVQALHQLYLSNKIETIPNGYFDPFPLAIRMYNKLIS--DRGLPRNS 283
 QY 239 ---PHLRELHNNKLTTRVPGGLAEHKYIQVYIHHNNISVVGSSDFCP 284
 DB 284 FDISNLVLHLSHNKISNP--ALSNKLEHLHNNISIEKINGIQIQCP 329

RESULT 12

08NC95 PRELIMINARY; PRT; 627 AA.

AC 08NC95; 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein FLJ90402.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

Query Match	20.0%;	Score 342;	DB 4;	Length 627;
Best Local Similarity	31.9%;	Pred. NO. 1.2e-15;		
Matches 90;	Conservative 49;	Mismatches 85;	Indels 58;	Gaps 9

	RESULT	13
OB8GT1		
ID	OB8GT1	PRELIMINARY; PRT; 649 AA.
AC	OB8GT1	
DT	01-MAR-2003	(TREMBlrel. 23, Created)
DT	01-MAR-2003	(TREMBlrel. 23, Last sequence update)
DT	01-MAR-2003	(TREMBlrel. 23, Last annotation update)
DE	Fibronectin leucine rich transmembrane protein 3 homolog.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
NCBI	NCBI_Taxid=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6J; TISSUE=Head, and Testis;	
RX	MEDLINE=22354683; PubMed=1246851;	
RA	The FANTOM Consortium,	
RA	the RIKEN Genome Exploration Research Group Phase I & II Team.	
RT	"Analysis of the mouse transcriptome based on functional annotation of	
RL	60,770 full-length cDNAs";	
RL	Nature 420:565-573(2002).	
EMBL	AK028252; BAC25843.1; -	
DR	EMBL; AK031464; BAC27417.1; -	

RESULT 14	
075093	
ID 075093	PRELIMINARY;
	PRT, 1534 AA.

DN 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-AUG-1999 (TREMBlrel. 11, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Slt-1 protein.
 GN Slt-1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99033071; PubMed=9813312;
 RA Itoh A., Miyabayashi T., Ohno M., Sakano S.;
 RT "Cloning and expressions of three mammalian homologues of dirosophila
 RT slt suggest possible roles for slt in the formation and maintenance
 of the nervous system.";
 RL Brain Res. Mol. Brain Res. 62:175-186(1998).
 DR EMBL; AB017167; BAA35184.1; -.
 DR HSSP; P00743; 1CCF.
 DR InterPro; IPR000152; Aa_x_hydroxyl.
 DR InterPro; IPR006207; Cys_knot_C.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR003645; FOLN.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR000372; LRR_Nterm.
 DR InterPro; IPR003591; LRR_cyp.
 DR Pfam; PF00008; EGF_9.
 DR Pfam; PF00054; laminin_G_1.
 DR Pfam; PF00560; LRR_19.
 DR Pfam; PF01463; LRRCT_4.
 DR Pfam; PF01462; LRRNT_4.
 DR PRINTS; PR00011; EGF_LAMININ.
 DR SMART; SMO0041; CT_1.
 DR SMART; SMO0179; EGF_CA_2.
 DR SMART; SMO0274; FOLN_3.
 DR SMART; SMO0282; LamG_1.
 DR SMART; SMO0082; LRRCT_4.

DR	SMART; SM00013; LRRNT; 4.
DR	SMART; SM00369; LRR_TYP; 10.
DR	PROSITE; PS00010; ASX_HYDROXYL; 2.
DR	PROSITE; PS01185; CTCK_1; 1.
DR	PROSITE; PS01225; CTCX_2; 1.
DR	PROSITE; PS00022; EGF_1; 9.
DR	PROSITE; PS01186; EGF_2; 8.
DR	PROSITE; PS01187; EGF_CA; 2.
DR	PROSITE; PS50025; LAM_G_DOMAIN; 1.
DR	PROSITE; PS50506; LRR_TYPICAL; 5.
DR	EGF-like domain.
SQ	SEQUENCE 1534 AA; 167952 MW; 8954EFBEADAEBAL CRC64;
Query Match	19.5%; Score 334.5; DB 4; Length 1534;
Best Local Similarity	25.1%; Pred.No. 13e-14;
Matches	97; Conservative 65; Mismatches 121; Indels 103; Gaps 9
Oy	10 VPDDRDF----BPSIGAPVCPFRCCQHRLRVQCSDGLDKVPKDLPPDTTLDLONNKITE 65
Dd	495 IPRGEDIYQLNSECNDVVCPEHKRCCEANVVECSSKLTKIPERITQSTAEHLANNNEISI 554
Oy	66 IK-DGDFFNLKNLHMLILVNKKISKVSFGAFTPLVKELRYLSKNQLKEPKMKPTIOE 124
Dd	555 LEATGMFKKLTHLKXINLNKKNSVSEIDQAFGAASVSELHTANQJESIRSGMFRGLDG 614
Oy	125 LRA--HENETTKVRKVTFNGLNQIVTVELGNPLKSGCIENGAFQMGKGS----- 173
Dd	615 LRITLMRNKRISCHINDSFCTLRNRLSLTDNYITT--VSPGADPTLOSISTLMILNP 672
Oy	174 ----- 173
Dd	673 FNCNCQLAMLGWLRKRKI VTGNPCQNBDPLRQI PLDDVAEPDFRCBGGEGCLPRP 732
Oy	174 -----YRIADTNITSIPQGLPPSLTEHLHDGKISRVDAAStKGNIHLAKGL 222
Dd	733 QCPEGCACLDIVVRSSNNKHIALPGIKRNVTELVDNGQPLTV-PGLSTFKYQLVNDL 791
Oy	223 SPNSISAVDNGSLANTPHLRLEHLDNKKLTRVE---GGLAEHKTYIQVYLHNNNISVVG 278
Dd	792 SNNKISSISNSFSFTWMSQTLTLLSYNALQCCIPPLAQGL--RSLRFLSLHGNDISTIQ 848
Oy	279 SSDPCPPGHNTKKASVGSVLSFSNV 304
Dd	849 EGIF-----ADVTSLSHALGANPL 868
RESULT 15	
O9UIL7	PRELIMINARY; PRT; 1618 AA.
ID	O9UIL7
AC	O9UIL7;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE	MEGF4 (Fragment).
GN	MEGF4.
OS	Homo sapiens (Human).
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Euteria; Primates; Carnivora; Homnidae; Homo.
OX	NCBI_Taxid=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISUB=Brain;
RC	MEDLINE=98360089; PubMed=9693030;
RA	Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
RT	"Identification of high-molecular-weight proteins with multiple EGF-
RT	-like motifs by motif-trap screening.";
RL	Genomics 51:27-34(1998).
DR	EMBL; AB011537; BAA32465.3; --
DR	HSSP; P00743; ICCP.
DR	GeneW; HGNC:11085; SLIT1.
DR	InterPro; IPRO00152; Asx_hydroxy1.
DR	InterPro; IPRO06207; Cys_kmot_C.
DR	InterPro; IPRO00742; EGF_2.

OY		InterPro; IPRO01881; EGF_Ca.
DR		InterPro; IPR001438; EGF_TL
DR		InterPro; IPR006209; EGF_1like.
DR		InterPro; IPR006210; IEGF.
DR		InterPro; IPR001791; Laminin_G.
DR		InterPro; IPR001611; LRR.
DR		InterPro; IPR000483; LRR_Cterm.
DR		InterPro; IPR000372; LRR_Nterm.
DR		InterPro; IPR003591; LRR_Typ.
DR	Pfam;	PF00008; EGF; 9.
DR	Pfam;	PF00054; Laminin_G; 1.
DR	Pfam;	PF00560; LRR; 19.
DR	Pfam;	PF01463; LRRC; 4.
DR	Pfam;	PF01462; LRRT; 4.
DR	PRINTS;	PRD0010; EGFBLD.
DR	PRINTS;	PRD0019; LEURICHRPT.
DR	SMART;	SMO0041; CT; 1.
DR	SMART;	SMO0181; EGF; 9.
DR	SMART;	SMO0179; EGF_CA; 9.
DR	SMART;	SMO0282; LamG; 1.
DR	SMART;	SMO0082; LRCT; 4.
DR	SMART;	SMO0013; LRNT; 4.
DR	SMART;	SMO0369; LRR_Typ; 18.
DR	PROSITE;	PS00010; ASX_HYDROXYL; 2.
DR	PROSITE;	PS01185; CTCCK_1; 1.
DR	PROSITE;	PS01225; CTCCK_2; 1.
DR	PROSITE;	PS00022; EGF_1; 9.
DR	PROSITE;	PS01186; EGF_2; 8.
DR	PROSITE;	PS01187; EGF_CA; 2.
DR	PROSITE;	PS50025; LAM_G_DOMAIN; 1.
DR	PROSITE;	PS50506; LRR_TYPICAL; 5.
DR	EGF-like domain.	
FT	NON TER	
SQ	SEQUENCE	1618 AA; 176732 MW; BF6ZDF0478B034E0 CRC64;
<hr/>		
Query Match 19.5%; Score 334.5; DB 4; Length 1618;		
Best local Similarity 25.1%; Pred. No. 1.4e-14; Indels 103; Gaps 9		
Matches 97; Conservative 65; Mismatches 121;		
OY	10 VPDDRDF----	EPISGLVCPFRCCCHLRVOCSDIGLDKVPKDLPPDTLLDLGNKKITE 65
DB	579 IPGEEDYOLNBECSDDVCHPKRCCEANVAVCSSKLTKIERIPQSIAELRLNNNEISI 638	
OY	66 IK-DGDPEKNILNALHILVNKISKVSQAFTPLVKERLYLSKNQLKEPDKMKTLOE 124	
DB	639 LEATGMFKGLTHLKIKINLNKRVSEIEDGAEGAASVELHTANQLSIRSGMRGLDG 698	
OY	125 LRA--HENETTYKRYKTFENGLNMIVLELTNPFLKSSGIENGAFQGKKLS----- 173	
DB	699 LRTLMRNRRISCIHNSDFTGIARVRVLISLYDNQITT--VSPGADTLQSLSTTNLANLP 756	
OY	174 -----	173
DB	757 FNQCQGLAMLGMLRKRIITYGNPRCONPDYLROIPLDVAFPDPFRCEGGEGGCLRP 816	
OY	174 -----YRIADNTITSIDGLEPSSLTEHLHDGNKISRVDAAISKLGNLIAGLGL 222	
DB	817 QCPOECACLDIVVACSNGHIALAPGPIKQVTLEYLDSNQITLV-PGLSTFYKQLVDL 875	
OY	223 SPNSISAVDNGSLANTPHILREHLHDNNKLTYP---GGLAEHKTIQVVYIHHNNISVVG 278	
DB	876 SNNKISSISNSSFTWMSQTLTILLISYNALOCIPIPAFOGL--RSLRLISLHGNDISTLQ 932	
OY	279 SSDPCFPGHNTKKASYSGVSLFSNPV 304	
DB	933 EGIF-----ADVTSLSHLAIGNPL 952	
<hr/>		
RESULT 16		
OBWA2 PRELIMINARY; PRT; 674 AA.		
ID	QBWA2	
AC	QBWA2;	
DT	01-MAR-2002 (TREMBLrel. 20, Created)	

DR SMART; SMO0274; FOLN; 2.
 DR SMART; SMO0282; Lamc; 1.
 DR SMART; SMO0082; LRCT; 4.
 DR SMART; SMO0013; LRENT; 4.
 DR SMART; SMO0369; LRR_TYP; 10.
 DR PROSITE; PS00010; ASX HYDROXYL; 2.
 DR PROSITE; PS01185; CTCK_1; 1.
 DR PROSITE; PS01225; CTCK_2; 1.
 DR PROSITE; PS00022; EGF_1; 9.
 DR PROSITE; PS01186; EGF_2; 8.
 DR PROSITE; PS50025; IAM G DOMAIN; 1.
 DR PROSITE; PS50506; LRR_TYPICAL; 5.
 KW EGF-like domain.

SO SEQUENCE 1531 AA; 167546 MW; F7D09AA6693A4F30 CRC64;

Query Match 19.2%; Score 328.5; DB 11; Length 1531;
 Best Local Similarity 24.5%; Pred. No. 3.3e-14;
 Matches 94; Conservative 65; Mismatches 127; Indels 97; Gaps 8

QY	10	VPPDRDF----	EPSIGPYCPFRQCCHLRVYCSDLGLDKVPKDLPEPDTLLDLQNNKITE	65
Db	495	IPGTEDYHINSECTSDVACPHKRCCEASVVECSIKLSKIPIRIPQSTTELRLANNNEISI	554	
QY	66	IK-DGDEFNLKNLHALILVNKKISKVSPGAFTPLVKLELYLSKNOKLPERMPPTLOE	124	
Db	555	LEATGLFKQLSHLKLNINSNNKVSSIEDOTFECAASVSFLHLTAQLESIRSGMFGIDG	614	
QY	125	LRA---HENETTKVAKVTFNGLNOMIVIELGNPLKSSGIEKGAFQMKKS-----	173	
Db	615	LRTLMRNKRISCHINDSFTGLRVRLSLSYDNHITT--ISFGAPDTLOALSTMLIANP	672	
QY	174	-----	173	
Db	673	FNCNGHLSWLGDWLARKRKIVTGNPRCQNPDPIRQIPLQVAFPPDFRCERGQEVGCLPRP	732	
QY	174	-----YIRADNRITSIPOGLPSLTETHLIDGKISRVDAAASKLANLAKTLGI	222	
Db	733	QCPDEACLDTPVRNSKNKLOALPKGIPKGVTELYIDGQFTLV-PGOLFSTFKLOLVVL	791	
QY	223	SFNSISAVDNGSLANTPHLRRLHLNNKKTLPVPG-GLAHKTIQVVYLNNNISVYGSSD	281	
Db	792	NNKLISSLSNSSFTNMSQULTTILSYNALOCIPPLAFQRLSRLLSLHGNDVSTIQEGI	851	
QY	282	FCPPGHNTKKAASYGSVISFSNPV	304	
Db	852	F-----ADVTSLSHLAIGANPL	868	

RESULT 19
 Q9WVB4 PRELIMINARY; PRT; 1523 AA.

ID	Q9WVB4	PRELIMINARY;	PRT;	1523	AA.
AC	O9WVB4:				
DT	01-NOV-1999	(TREMBLrel. 12, Created)			
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)			
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)			
DE	Slit3 (Fragment).				
GN	Slit3.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCB1_TaxId=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Swiss Webster/ICR.				
EX	MEDLINE=99365246; PubMed=10433822;				
FA	Yuan W., Zhou L., Chen J.H., Wu J.Y., Rao Y., Ornitz D.M.,				
RT	"The mouse Slit family: secreted ligands for ROBO expressed in				
RL	patterns that suggest a role in morphogenesis and axon guidance.";				
RD	Dev. Biol. 212:290-306(1999).				
DR	EMBL; AF144629; AAD44760.1; --				
DR	HSSB; P01132; IEGB.				
DR	MGD; MG1:J315202; Slit3.				

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DR InterPro:IPR000153; Asx_hydroxyl.
DR InterPro:IPR006207; Cys_knuc_C.
DR InterPro:IPR000742; EGF_2.
DR InterPro:IPR001881; EGF_Ca.
DR InterPro:IPR001438; EGF_II.
DR InterPro:IPR006209; EGF_III.
DR InterPro:IPR002049; laminin_EGF.
DR InterPro:IPR001791; laminin_G.
DR InterPro:IPR001611; LRR.
DR InterPro:IPR000483; LRR_Cterm.
DR InterPro:IPR000372; LRR_Nterm.
DR InterPro:IPR003591; LRR_typ.
DR Pfam:PF00008; EGF_9.
DR Pfam:PF00054; laminin_G; 1.
DR Pfam:PF00560; LRR; 19.
DR Pfam:PF01463; LRRCT; 4.
DR Pfam:PF01462; LRRNT; 4.
DR PRINTS:PRO0010; EGBLOOD.
DR PRINTS:PRO0011; EGBLAMININ.
DR PRINTS:PRO0019; LEURICHRPT.
DR SMART:SM00041; CT; 1.
DR SMART:SM00179; EGF_CA; 1.
DR SMART:SM00282; lamg; 1.
DR SMART:SM00082; LRRCT; 4.
DR SMART:SM00013; LRRNT; 4.
DR SMART:SM00369; LRR_TYP; 7.
DR PROSITE:PS00010; ASX_HYDROXYL; 2.
DR PROSITE:PS01185; CTCK_1; 1.
DR PROSITE:PS01225; CTCK_2; 1.
DR PROSITE:PS00023; EGF_1; 9.
DR PROSITE:PS01186; EGF_2; 7.
DR PROSITE:PS01187; EGF_CA; 1.
DR PROSITE:PS05025; LAM_G_DOMAIN; 1.
DR PROSITE:PS05006; LRR_TYPICAL; 5.
KW EGF-like domain.
FT NON TER 1523
SQ SEQUENCE 1523 AA; 167711 MW; F42A3F3E016C4BFC CRC64;

Query Match 19.1%; Score 328; DB 11; Length 1523;
Best Local Similarity 24.9%; Pred. No. 3.5e-14;
Matches 99; Conservative 53; Mismatches 124; Indels 122; Gaps 7.

QY 21 GF---VCPFCQCHLRVYQSDLGIDKVPKDLPPDTLLDQNNKITEIKDGFKNLKL 77
DB 28 GPAAACPTKCTCSAAVSDCGLGLRAVPRGI PNNAERLIDRRNNITPTKQDFAGLNKL 87
QY 78 HALLVNNKTSKVSFGAFTPLVKLERLYLSKNOLKEPEKM-----PKTQELRAHENEIT 133
DB 88 RVLLENDQVSIIRGAFODIKQLERLRLNNKIQVPELTFPOSTPK-LTRIDUSENOIQ 146
QY 134 KVRKVTFGNLQMTIVIEIGTNPILKSSGIENGAFQGMKKLSYIRLADTNI----- 182
DB 147 GIPKARRGVGVGNLDQNDNHI--SCIEDAFALNRLLELTLNNNNISSILVTSFNHM 204
QY 183 ----- 182
DB 205 PKIRTLRLSHNHLCDCHLAWLSDMLRQRRTIGQFTLCMAEVLHGFSAVDQKKEYYCP 264
QY 183 -----TSTPQGLPRSLTEHLHGKTSRYDA 208
DB 265 GPHSEAPACNANSLSCPASCSNNIVDCRKGLELPANLPPEGIVLRLEONSITKSIPA 324
QY 209 ASLGLNNLIALGLSFNSISAVDNGSLANTPHLEIRLHDNNKLFEVPGSLAEHKY-IQV 267
DB 325 GAFVQYKKLAKRIDISKNOISDIADAPQGLKSLTSIVLYGNKKITEIPKGLDPGLVSLQL 384
QY 268 YLHNNNISVVGSSDPFCPPGHNTKASVGSGLFSNPVO 305
DB 385 LLNANKINCLRVNTE-----QDLQNLNLTSLYDNKIQ 416

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ID 088279 PRELIMINARY; PRT; 1531 AA.
AC 088279;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE MEGF4.
GN MEGF4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=98360089; PubMed=9693030;
RA Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
RT "Identification of high-molecular-weight proteins with multiple EGF-
RT like motifs by motif-trap screening.";
RL Genomics 51:27-34(1998).
DR EMBL/AB011530; BAA32460.1; -.
DR HSSP; P00743; IAP0.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR006207; Cys_knot_C.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR003645; F0LN.
DR InterPro: IPR002049; Laminin_EGF.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR000372; LRR_Nterm.
DR Pfam: PF00008; EGF_9.
DR Pfam: PF00054; laminin_G_1.
DR Pfam: PF00560; LRR_19.
DR Pfam: PF01463; LRRCT; 4.
DR Pfam: PF01462; LRRNT; 4.
DR PRINTS; PR00011; EGF_LAMININ.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_CA_2.
DR SMART; SM00274; F0LN; 3.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00082; LRRCT; 4.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_TYP; 10.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01185; CTCK_1; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS01187; EGF_CA_2.
DR PROSITE; PS50025; LAM_G_DOMAIN; 1.
DR PROSITE; PS50506; LRR_TYPICAL; 5.
KW EGF-like domain.
SQ
SEQUENCE 1531 AA; 167497 MW; DFC4860CCBC5529A CRC64;

Query Match 19.1%; Score 327.5; DB 11; Length 1531;
Best Local Similarity 24.9%; Pred. No. 3.9e-14;
Matches 96; Conservative 65; Mismatches 122; Indels 103; Gaps 9;

QY 10 VPDPRDF-----EPLGLVCFPRCCCHLRVYVQCSDLGLDKYKDLPPPTLLDQNNKITE 65
DB 495 IPGTEHYHLSNCTSDVACPHCKRCCEASVVEGSLGSKIPERIPSTELRLNNNEIST 554
QY 66 IK-DGDPKATKATHALILVNNKISKVSPGAFPLVVKLERLYLSKNQKELPEKKPKTLQE 124
DB 555 LEATGTFPKLSHKKNLNNKXSELEDGTFEGATVSEELHTANQLESYRSGWFRGLDG 614
QY 125 LRA---HNEITKRVKTFNGLNQMVYIELGTNPDKSGIENGAFQGMKKLS----- 173
DB 615 LRTLMRNRRNISCHINDSFTGLKRVRLSLYDNHITT--ISPGAFDTLQALSTLNLAMP 672

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QY 174 ----- 173
DB 673 FNCNCQALWGLDKLRKKKIVTGNPRQNPFLNQLPIQDVAFPDFRCEBGEQEVGLPRP 732
QY 174 -----YRIADTNITSIPQGLPSELTLHDGKISKVDAASLGLNNLAKLGL 222
DB 733 QCPQECACLDPTVRCNKHQLQALPKGIPKVTBELYLDGNQFTLV-PCQLSTPKYLQAVDL 791
QY 223 SFNSISAVDNGSLANPRLRELLDNNKLTFRP-----GGLAEKTYIQVYTHNNNISVVG 278
DB 792 SNNKISSLSNSFTNNSQLTTLTSLYNAQCIPPLAFQGL--RSRLSLSLHGNDVSTLQ 848
QY 279 SSDPCPEGHNTKKASYSVGSVLFSPNPV 304
DB 849 EGF-----ADVTSLSHLAGNPL 866

RESULT 21
ID 088280 PRELIMINARY; PRT; 1523 AA.
AC 088280;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE MEGF5.
GN MEGF5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=98360089; PubMed=9693030;
RA Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
RT "Identification of high-molecular-weight proteins with multiple EGF-
RT like motifs by motif-trap screening.";
RL Genomics 51:27-34(1998).
DR EMBL/AB011531; BAA32461.1; -.
DR HSSP; P01132; IEGF.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR006207; Cys_knot_C.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_I1.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR002049; Laminin_EGF.
DR InterPro: IPR001791; Laminin_G.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR003591; LRR_Nterm.
DR Pfam: PF00008; EGF_9.
DR Pfam: PF00054; laminin_G_1.
DR Pfam: PF00560; LRR_19.
DR Pfam: PF01463; LRRCT; 4.
DR Pfam: PF01462; LRRNT; 4.
DR PRINTS; PR00010; EGF_LIGAND.
DR PRINTS; PR00011; EGF_LAMININ.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_CA_1.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00082; LRRCT; 4.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_TYP; 9.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01185; CTCK_1; 1.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS01187; EGF_CA_2.
DR PROSITE; PS50025; LAM_G_DOMAIN; 1.

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GN	SIFT2.	
OC	Brydnamio rerio (Zebrafish)	(Danio rerio).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	
OC	Cyprinidae; Danio.	
OX	NCBI_TaxID=7955;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Michigan;	
RA	Yeo S.Y., Okamoto H.;	
RL	"Zebrafish slt2 homolog."	
RT	Submitted (DEC-1999) to the EMBL/DDBJ databases.	
DR	EMBL; AF210321; AAC36773.1; -	
DR	HSSP; P00740; 1EDM	
DR	ZFIN; ZDB-GENE-010306-3; slt2.	
DR	InterPro; IPR000152; Asx_Hydroxyl.	
DR	InterPro; IPR006207; Cys_knot_C.	
DR	InterPro; IPR000742; EGF_2.	
DR	InterPro; IPR001881; EGF_Ca.	
DR	InterPro; IPR001438; EGF_1T.	
DR	InterPro; IPR006209; EGF_like.	
DR	InterPro; IPR003645; FOLN.	
DR	InterPro; IPR001791; Laminin_G.	
DR	InterPro; IPR001611; LRR.	
DR	InterPro; IPR000483; LRR_Cterm.	
DR	InterPro; IPR000372; LRR_Nterm.	
DR	InterPro; IPR003591; LRR_tyr.	
DR	Pfam; PF00008; EGF; 9. _typ.	
DR	Pfam; PF00054; laminin_G; 1.	
DR	Pfam; PF00560; LRR; 18.	
DR	Pfam; PF01463; LRCT; 4.	
DR	Pfam; PF01462; LRNT; 4.	
DR	PRINTS; PR00010; EGFBLLOOD.	
DR	PRINTS; PR00019; LEURICHRPT.	
DR	SMART; SM00041; CT; 1.	
DR	SMART; SM00179; EGF_CA; 2.	
DR	SMART; SM00274; FOLN; 2.	
DR	SMART; SM00282; LamG; 1.	
DR	SMART; SM00082; LRCT; 4.	
DR	SMART; SM00013; LRNT; 4.	
DR	SMART; SM00369; LRR_TYP; 8.	
DR	PROSITE; PS00010; ASX_HYDROXYL; 2.	
DR	PROSITE; PS01185; CTCK_1; 1.	
DR	PROSITE; PS01225; CTCK_2; 1.	
DR	PROSITE; PS00022; EGF_1; 9.	
DR	PROSITE; PS01186; EGF_2; 8.	
DR	PROSITE; PS01187; EGF_CA; 2.	
DR	PROSITE; PS00025; LAM_G_DOMAIN; 1.	
DR	PROSITE; PS05006; LRR_TYPICAL; 4.	
KW	EGF-like domain.	
SW	SEQUENCE 1512 AA; 16669 MW; 608888CQAFCCD30 CRC64;	
Query Match	19.0%; Score 325; DB 13; Length 1512;	
Best Local Similarity	24.7%; Pred. No. 5.7e-14;	
Matches 98; Conservative	54; Mismatches 129; Indels 116; Gaps	6
QY	24 CPFRCOCHTRVVOCSDLGLDKVPKQLPDDTLTDIQQNKTEIRIKDGDFNLKNLALILIV	83
DQ	21 CPSCGSGSGTVADHCGQSRLSVPRNIPRNVERLDIMANNLTITTTADPAGLNKLVLQLM	80
QY	84 NNKISKVSFGAFTPLVKLERLYLSRNOUKELPEKM--PKTLQELPAHENETTKVRKYTF	140
DQ	81 ENKISIERGAFOQLQELERLRINNNNQVPELLFLGTGKLFRLDSLSENQIGIPRKAF	140
QY	141 NGNLQMVLIELGTPIPLSSGIENGAFQGMKKLSYRIADPTNI-----	182
DQ	141 RGSYEIKVLQLDYNOT--SCIEDGAFFRALGDLEVTLLNNNNISRLSVASFNMPPKLRTER	198
QY	183 -----	182
DQ	199 LHSNNLLCDNCVAVMLSDWLQRPRRLGLTYQCACAPSLAGHNIAFYOKKEPFMTGPQSHSS	258
QY	183 -----TSIFOGLPSPSITEHLHDGNKISRVDASLKGKLANLIA	218

Db	259	CSVLQCPCLCTCSNNVVDRCGKGLVEITPTNIPETITETRELQNSIKIKIIPAGAPFPRKLR	318
Qy	219	KCLSLSNLSIAVDNGLSLANTPLRLHLDDNNKLTFRVGGLAEHKY-IQVYLLHNNTISV	277
Db	319	RIDLNNQITTELASDFSQGLRLSLVLYGKIKITELPKGLFDGULSLQLLLNANKINCL	378
Qy	278	GSSDFPCPGHNTKKASYSVSLFSNPVQYWEIQTSTF	314
Db	379	RVDSE-----QDLQNLNMLSLYDNKLG--ITIAGTG	407
RESULT 24			
075094			
ID	075094	PRELIMINARY;	PRT; 1523 AA.
AC	075094;		
DT	01-NOV-1998	(T-EMBLrel. 08, Created)	
DT	01-NOV-1999	(T-EMBLrel. 11, Last sequence update)	
DT	01-MAR-2003	(T-EMBLrel. 23, Last annotation update)	
DE	SLIT-3 protein (MEGFS).		
GN	SLIT-3 OR MEGF5.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=99033071; PubMed=9813312;		
RA	Itch A., Miyabayashi T., Ohno M., Sakano S.;		
RT	"Cloning and expressions of three mammalian homologues of Drosophila		
RT	slit suggest possible roles for Slit in the formation and maintenance		
RL	of the nervous system."		
RL	Brain Res. Mol. Brain Res. 62:175-186(1998).		
RN	[2]		
RP	SEQUENCE OF 785-1523 FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE=98360089; PubMed=9693030;		
RA	Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;		
RT	"Identification of high-molecular-weight proteins with multiple EGF-		
RT	like motifs by motif-trap screening."		
RL	Genomics 51:27-34(1998).		
DR	EMBL: AB017169; BAA35186.1; -		
DR	EMBL: AB011538; BAA32466.1; -		
DR	HSSP; P00740; 1EDM.		
DR	Genew; HGNC:11087; SLIT3.		
DR	InterPro; IPR000152; Asx hydroxyl.		
DR	InterPro; IPR006207; Cys knot_C.		
DR	InterPro; IPR000742; EGF_2.		
DR	InterPro; IPR001881; EGF_Ca.		
DR	InterPro; IPR006209; EGF_like.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR001791; Laminin_G.		
DR	InterPro; IPR001611; LRR.		
DR	InterPro; IPR000483; LRR_Cterm.		
DR	InterPro; IPR000372; LRR_Nterm.		
DR	InterPro; IPR003591; LRR_typ.		
DR	Pfam; PF00008; EGF; 9.		
DR	Pfam; PF00054; laminin_G; 1.		
DR	Pfam; PF00560; LRR; 19.		
DR	Pfam; PF01463; LRRCT; 4.		
DR	Pfam; PF01462; LRRNT; 4.		
DR	PRINTS; PRO0019; LEURICHRPT.		
DR	SMART; SM00041; CT; 1.		
DR	SMART; SM00179; EGF_CA; 1.		
DR	SMART; SM00282; LamG; 1.		
DR	SMART; SM00082; LRRCT; 4.		
DR	SMART; SM00013; LRRNT; 4.		
DR	SMART; SM00369; LRR_TYP; 9.		
DR	PROSITE; PS00010; ASX_HYDROXYL; 2.		
DR	PROSITE; PS01185; CTCK_1; 1.		
DR	PROSITE; PS01225; CTCK_2; 1.		
DR	PROSITE; PS00022; EGF_1; 9.		
DR	PROSITE; PS00186; EGF_2; 7.		

Qy 279 SSDPCPGHNTKASYSVSLFSPNV 304
Db 849 EGIF-----ADVTSLHLAGANPL 868

RESULT 27

ID 094813 PRELIMINARY; PRT; 1529 AA.
AC 094813;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Slt-2 protein.
GN Slt-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=99033071; PubMed=9813312;
RA Itoh A., Miyabayashi T., Ohno M., Sakano S.;
RT "Cloning and expressions of three mammalian homologues of drosophila
RT slt suggest possible roles for slt in the formation and maintenance
RT of the nervous system."
RL Brain Res. Mol. Brain Res. 62:175-186(1998).
DR EMBL; AB017168; BAA35185.1; -.
DR HSPB; P00743; IICF.
DR Genew; HGNC:11086; Slt2.
DR InterPro; IPR000152; Aax_hydroxyl.
DR InterPro; IPR006207; Cys_knot_C.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR003645; PolN.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR00372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Cyp.
DR Pfam; PF00008; EGF; 9.
DR Pfam; PF00054; laminin_G; 1.
DR Pfam; PF00560; LRR; 17.
DR Pfam; PF01463; LRRT; 4.
DR Pfam; PF01462; LRRT; 4.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00274; POLN; 2.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00082; LRRT; 4.
DR SMART; SM00013; LRRT; 4.
DR SMART; SM00369; LRR_Typ; 8.
DR PROSITE; PS00010; AAX_HYDROXYL; 2.
DR PROSITE; PS01185; CTCK_1; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00025; LAM_G_DOMAIN; 1.
DR PROSITE; PS05006; LRR_TYPICAL; 5.
DR EGF-like domain.
SQ SEQUENCE 1529 AA; 169869 MW; 5D19C5E7FD461BA CRC64;

Query March 18.8%; Score 322; DB 4; Length 1529;
Best Local Similarity 25.2%; Pred. No. 9.3e-14;
Matches 104; Conservative 62; Mismatches 129; Indels 118; Gaps 12;

Qy 10 VPDDRDEPSPISGP-----VCPFRCCQLIRVVOCSDLGLDKVPKDLPPDTTLDLONNKI 63
Db 486 IPGTEDEYRSKLSGCGPDLACPEKRCRCGCTVDGSGNOLANKIPHHIPYTLALANNEF 545
Qy 64 TEIK-DGDFKULKULHALLIVNNKISKVSPGAFPLVLEKRLYLSKNQKELPEKMPKYL 122

Db 546 TVLEATGIFFKLPOLRKINFSNNKITDIEGAFEGASGVVEILLTENVGQKMKGL 605
Qy 123 QELRA-----HENETKRYKTYTNLQMIYELGTNP 155
Db 606 ESUKTLMRLSRNRTVCVNDSEFGLSVRLISLYDNOITTVAPAPAFDTLSLTNLINAP 665
Qy 156 -----LKSGIENGAPQ-----GMKLS 173
Db 666 FNCNCYIAMIIEWLKRKKRIYVGNPROCKPYFLKEIPIDVAIDFTCDGNDNDSCEPLS 725
Qy 174 -----YRIADTNITSIPQGLPSLTELHDGNKI SRVDAASLGLNNLALYGL 222
Db 726 RCPTECTCLDTVVRCSNKGILKVLPGKIPRDVTELYLDGNQFTLV-PRKLSNYKHLTLIDL 784
Qy 223 SPSISAVDNGSLANPRLHELHDNNKILTRVP-----GGLAEKTYIQVYVLANNTSYVG 278
Db 785 SNNRISTLSNQSFSNNQTLLTLISYRRLKCIPTPTFDGL--KSLRLSLHGNDSIVV- 840
Qy 279 SSDPCPGHNTKASYSVSLFSPNV-----QYMEIOPSTFRC 316
Db 841 -----PGAFNDLSALSHLAGANPLXCDCNMGLSDWVSEYKE--PGIARC 886

RESULT 28

ID 081V47 PRELIMINARY; PRT; 376 AA.
AC 081V47;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Similar to fibromodulin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RC Strausberg R.;
RA Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.
RL EMBL; BC035281; AAB35281.1; -.
SQ SEQUENCE 376 AA; 43178 MW; DC19D5E6724AB004 CRC64;

Query March 18.8%; Score 321.5; DB 4; Length 376;
Best Local Similarity 29.9%; Pred. No. 1.7e-14;
Matches 85; Conservative 55; Mismatches 119; Indels 25; Gaps 8;

Qy 8 PEVDDRDEPSPISGPVCPFRCC--HLRVVOCSDLGLDKVPKDLPPDTTLDLONNKIT 64
Db 68 PSPDPDR-----CPQECDCPPNPFTAMVCDNNNLKYL-FVPSRMKYVVFQNNQIT 118
Qy 65 EIKDGPKNLKNLHALLIVNNKIS--KVSQAFPLVLEKRLYLSKNQKELPEKMPKYL 122
Db 119 SIQGVFDNATGLMTALHNOITSDKVGKVSFKRHLERLYLDHNNLTRMGPLPRSL 178
Qy 123 QELRAHENETTKRYKTYTNLQMIYELGTNPLKSGIENGAFQGMKLSYRIADTNI 182
Db 179 RELHLHDNQSRYPNNAALSGLENTLYLDHANIQYGV--SSMRGLRSLLILDSTNHL 235
Qy 183 TSIPQGLPSLTELHDGNKISRVDASLGLNNLAKGLSFSNISAVDNGSLANT--P 239
Db 236 RKVPDGLPSALBEDLYMEHNNVYVPPSYPGAPKLYLVRSNHSLT--NNGLASNTNNS 293
Qy 240 HLEBLHDNNKILTRVQGLAEHKYIQVYVLANNTSYVSGSSDPC 283
Db 294 SLTELDSLNYQLQKIP---PVNTNLEMLYLDGNRINEFSSISC 334

RESULT 29
Q9DE37 PRELIMINARY; PRT; 1515 AA.
ID Q9DE37
AC Q9DE37;

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DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE SLIT3.
GN SLIT3.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Michigan;
RA Yeo S.Y., Okamoto H.;
RT "Zebrafish slit3 homolog.";
RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF210320; AAG36772.1; -.
DR HSSP; P00740; 1EDM.
DR ZFIN; ZDB-GENE-010306-4; slit3.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR006207; Cys_knot_C.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00008; EGF_9.
DR Pfam; PF00054; laminin_G_1.
DR Pfam; PF00560; LRR_18.
DR Pfam; PF01463; LRRCT; 4.
DR Pfam; PF01462; LRRNT; 4.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_Ca; 1.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00082; LRRCT; 4.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_Typ; 9.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01185; CTCK_1; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS01187; EGF_Ca; 2.
DR PROSITE; PS50025; LAM_G_DOMAIN; 1.
DR PROSITE; PS50506; LRR_TYPICAL; 5.
DR EGF-like domain.
KW EGF-like domain.
SQ SEQUENCE 1515 AA; 166871 MW; 12FD11277D18D5B CRC64;

Query Match 18.6%; Score 318.5; DB 13; Length 1515;
Best Local Similarity 22.4%; Pred. No. 16e-13;
Matches 100; Conservative 53; Mismatches 133; Indels 161; Gaps 7;

QY 24 CEFRCQCHLRVYQCSGLDGLDKVPKLPDPTLLDLONNKITEIKQDFKTLKNTLALIV 83
DB 24 CPHKSCSGSHVDCQQAFAKTVPRGIPRAVERLDIDRNNITITTKVDFGLKNTLALHLE 83
QY 84 NKKIKSVGATPLVYKLERLYLSKQKLEPEKPKMT--LOELRAHENEITTKRATVP 140
DB 84 NNQISVIERGAEFGKQKLERIRLNRRLOVLPBLFQSTTKLSRLDLSNQIOAVPRKAF 143
QY 141 NGINQIVIELGTNPPLKSSGIENGAFQGGKKLSYIRIADTNI----- 182
DB 144 RQITTVKXKLQSDSNHI--SCIEDGAFRALRDLEILTNNNNTITLPLSSFNMPKLTIR 201
QY 183 ----- 182
DB 202 LHSNNLHCDCHLSWLSDWLRQRRLGLAFTQCVAPAMRGILAVDVQKREFTCTGVETEP 261
QY 183 -----TSIQGLPPSLTEHLSDNKISRDPAASLKL 214

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DB 262 RSCAQATTCIPACTCANNIYDCKRKGLTEIRPANIPEGVETRLQONMKNIPAGAFSTY 321
QY 215 NNIAKLGISFNSISAVDNGSLANTPHLEHLDDNKKLTRVPGGL----- 258
DB 322 KKLKRDISSKQISIEADAFGLSLSLVLYGKKIAEIPGLFGLVSLQLLLLNANK 381
QY 259 -----AEKTYQVYTHHNNNISVVGSSDFC-----FGHTKKAS 293
DB 382 INCLRVNTEFKDLQNLNLSLDNKKQTISKGLFAPLRAIKTLHLAQNPFMCDCHLKMILAD 441
QY 294 YSGVSLFSNPVQVWEIOPSTPFCVYVR 320
DB 442 Y-----LFDNP-----LETSGARCSHPR 459

RESULT 30
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AC O991B9,
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE SLIT2.
GN SLIT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster/ICR;
RA MEDLINE=99365246; PubMed=10433822;
RA Yuan W., Zhou L., Chen J.H., Wu J.Y., Rao Y., Ornitz D.M.;
RT "The mouse Slit family: secreted ligands for ROBO expressed in
RT patterns that suggest a role in morphogenesis and axon guidance.";
RL Dev. Biol. 212:290-306(1999).
DR EMBL; AF144628; AAD4759.1; -.
DR HSSP; P00743; 1CCF.
DR MGD; MGI:1315205; Slit2.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR006207; Cys_knot_C.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR003645; FOIN.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Typ.
DR Pfam; PF00008; EGF_9.
DR Pfam; PF00054; laminin_G_1.
DR Pfam; PF00560; LRR_17.
DR Pfam; PF01463; LRRCT; 4.
DR Pfam; PF01462; LRRNT; 4.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_Ca; 2.
DR SMART; SM00274; FOIN; 2.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00082; LRRCT; 4.
DR SMART; SM00013; LRRNT; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01185; CTCK_1; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS01187; EGF_Ca; 2.
DR PROSITE; PS50025; LAM_G_DOMAIN; 1.
DR PROSITE; PS50506; LRR_TYPICAL; 5.
DR EGF-like domain.
KW EGF-like domain.
SQ SEQUENCE 1521 AA; 168769 MW; 97DCA361578978E4 CRC64;

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OM protein - protein search, using sw model

Run on: February 9, 2004, 11:38:24 / Search time 75 Seconds

(without alignments)
918.490 Million cell updates/sec

Title: US-10-004-176-6

Perfect score: 1713

Sequence: 1 VASGIGPEVDDRDPEPSL.....QPTFRVCVYSAIQGNK 329

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1713	100.0	329	US-10-004-176-6	Sequence 6, Appl1
2	1709	99.8	360	US-09-764-875-804	Sequence 804, App
3	1365.5	79.7	354	US-10-319-130-20	Sequence 20, Appl
4	984.5	57.5	369	US-10-319-130-19	Sequence 19, Appl
5	979	57.2	368	US-10-236-031B-68	Sequence 68, Appl
6	979	57.2	368	US-10-177-253-99	Sequence 29, Appl
7	943.5	55.1	379	US-09-866-028-2	Sequence 2, Appl1
8	943.5	55.1	379	US-09-944-449-2	Sequence 2, Appl1
9	943.5	55.1	379	US-09-944-457-2	Sequence 2, Appl1
10	943.5	55.1	379	US-09-944-862-2	Sequence 2, Appl1
11	943.5	55.1	379	US-09-945-587-2	Sequence 2, Appl1
12	943.5	55.1	379	US-09-945-015-2	Sequence 2, Appl1
13	943.5	55.1	379	US-09-944-396-2	Sequence 2, Appl1
14	943.5	55.1	379	US-09-944-097-2	Sequence 2, Appl1
15	943.5	55.1	379	US-09-944-432-2	Sequence 2, Appl1

16	943.5	55.1	379	US-09-943-762-2	Sequence 2, Appl1
17	943.5	55.1	379	US-09-944-654-2	Sequence 2, Appl1
18	943.5	55.1	379	US-09-943-851A-2	Sequence 2, Appl1
19	943.5	55.1	379	US-09-944-413-2	Sequence 2, Appl1
20	943.5	55.1	379	US-09-944-403-2	Sequence 2, Appl1
21	943.5	55.1	379	US-09-944-896-2	Sequence 2, Appl1
22	943.5	55.1	379	US-09-944-929-2	Sequence 2, Appl1
23	943.5	55.1	379	US-09-944-929-2	Sequence 2, Appl1
24	943.5	55.1	379	US-09-944-907-2	Sequence 2, Appl1
25	943.5	55.1	379	US-09-944-884-2	Sequence 2, Appl1
26	943.5	55.1	379	US-09-944-852-2	Sequence 2, Appl1
27	943.5	55.1	379	US-09-943-780-2	Sequence 2, Appl1
28	943.5	55.1	379	US-10-137-870-328	Sequence 328, App
29	943.5	55.1	379	US-10-140-018-328	Sequence 328, App
30	943.5	55.1	379	US-10-140-021-328	Sequence 328, App
31	943.5	55.1	379	US-10-140-274-328	Sequence 328, App
32	943.5	55.1	379	US-10-140-471-328	Sequence 328, App
33	943.5	55.1	379	US-10-140-807-328	Sequence 328, App
34	943.5	55.1	379	US-10-140-922-328	Sequence 328, App
35	943.5	55.1	379	US-10-140-924-328	Sequence 328, App
36	943.5	55.1	379	US-10-140-926-328	Sequence 328, App
37	943.5	55.1	379	US-10-141-698-328	Sequence 328, App
38	943.5	55.1	379	US-10-141-702-328	Sequence 328, App
39	943.5	55.1	379	US-10-141-704-328	Sequence 328, App
40	943.5	55.1	379	US-10-142-421-328	Sequence 328, App
41	943.5	55.1	379	US-10-142-432-328	Sequence 328, App
42	943.5	55.1	379	US-10-142-767-328	Sequence 328, App
43	943.5	55.1	379	US-10-143-033-328	Sequence 328, App
44	943.5	55.1	379	US-10-144-994-328	Sequence 328, App
45	943.5	55.1	379	US-10-145-628-328	Sequence 328, App

ALIGNMENTS

RESULT 1
US-10-004-176-6
; Sequence 6, Application US/10004176
; Publication No. US20030124152A1
; GENERAL INFORMATION:
; APPLICANT: Pang, Danny Z.
; TITLE OF INVENTION: Use of decorin in a cosmetic or dermatological composition
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/004,176
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 6
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Human
US-10-004-176-6

Query Match 100.0%; Score 1713; DB 15; Length 329;
Best Local Similarity 100.0%; Pred. No. 2.6e-152;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	VEASGIGPEVDDRDPEPSLGPVCPFRQCHRVQCSDDLGLDKVPKDLPPDTILLDION	60
DB	1	VEASGIGPEVDDRDPEPSLGPVCPFRQCHRVQCSDDLGLDKVPKDLPPDTILLDION	60
QY	61	NKITEIKQGDPRKNTKNTALILVNNKTSKVSFGAFTPLVKLERLYLSKNOIKELPEKMPK	120
DB	61	NKITEIKQGDPRKNTKNTALILVNNKTSKVSFGAFTPLVKLERLYLSKNOIKELPEKMPK	120
QY	121	TLQELRAHENEITTKRVKTFNGLNQMTVIELGTNPLKSSGIEENGAFQCKKLSTYRIADT	180
DB	121	TLQELRAHENEITTKRVKTFNGLNQMTVIELGTNPLKSSGIEENGAFQCKKLSTYRIADT	180
QY	181	NITSIPQGLPSLTLEHDKNKISRVDASIKGLNNLAKLGLSFNISAIVNGSLANTPH	240
DB	181	NITSIPQGLPSLTLEHDKNKISRVDASIKGLNNLAKLGLSFNISAIVNGSLANTPH	240

QY 241 LRELHNNKLTTRVPGGLAEHKYIOVVYLLNNNISVVGSSDPFGPHNTKASYSVSLP 300
 DB 241 LRELHNNKLTTRVPGGLAEHKYIOVVYLLNNNISVVGSSDPFGPHNTKASYSVSLP 300
 QY 301 SNPVOYWEIQPSTFRVCVYRSAIQLGNYK 329
 DB 301 SNPVOYWEIQPSTFRVCVYRSAIQLGNYK 329

RESULT 2

US-09-764-875-804
 ; Sequence 804, Application US/09764875
 ; Publication No. US20040018969A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: P3202
 ; CURRENT APPLICATION NUMBER: US/09/764,875
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 1249
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 804
 ; LENGTH: 360
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-764-875-804

Query Match 99.8%; Score 1709; DB 12; Length 360;
 Best Local Similarity 100.0%; Pred. No. 6,9e-152;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EASGIGPEVDDRDPEPSIGPVCPFCQCHLRVQCSDGLDKVPRDLPDPTLLDLQNN 61
 DB 33 EASGIGPEVDDRDPEPSIGPVCPFCQCHLRVQCSDGLDKVPRDLPDPTLLDLQNN 92
 QY 62 KITTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLERLYLSKNQKELPERKMPKT 121
 DB 93 KITTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLERLYLSKNQKELPERKMPKT 152
 QY 122 LOELRAHENEITKRVKVTENGNGNOMIVIELGTNPPLKSSGIENGAFQGMKQLSYIRIADTN 181
 DB 153 LOELRAHENEITKRVKVTENGNGNOMIVIELGTNPPLKSSGIENGAFQGMKQLSYIRIADTN 212
 QY 182 ITSIPQGLPSTLTELHLDGNKISRVDASLKGILNLAQLGSLFNSISAVDNGSLANTPHL 241
 DB 213 ITSIPQGLPSTLTELHLDGNKISRVDASLKGILNLAQLGSLFNSISAVDNGSLANTPHL 272
 QY 242 RELHLDNNKLTTRVPGGLAEHKYIOVVYLLNNNISVVGSSDPFGPHNTKASYSVSLP 301
 DB 273 RELHLDNNKLTTRVPGGLAEHKYIOVVYLLNNNISVVGSSDPFGPHNTKASYSVSLP 332
 QY 302 NPVOYWEIQPSTFRVCVYRSAIQLGNYK 329
 DB 333 NPVOYWEIQPSTFRVCVYRSAIQLGNYK 360

RESULT 3

US-10-319-130-20
 ; Sequence 20, Application US/10319130
 ; Publication No. US20030148351A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Henry, Stephen P
 ; APPLICANT: Mayne, Richard
 ; APPLICANT: Hook, Magnus
 ; TITLE OF INVENTION: NUCLEIC ACID AND PROTEIN SEQUENCES OF ASPORINS
 ; FILE REFERENCE: 12740.0234.NPUS02
 ; CURRENT FILING DATE: 2002-12-13
 ; CURRENT APPLICATION NUMBER: US/10/319,130
 ; PRIOR APPLICATION NUMBER: US 60/341,537
 ; PRIOR FILING DATE: 2001-12-13
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 20
 ; LENGTH: 354
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-319-130-20

Query Match 79.7%; Score 1365.5; DB 12; Length 354;
 Best Local Similarity 79.9%; Pred. No. 1.2e-119;
 Matches 262; Conservative 28; Mismatches 33; Indels 5; Gaps 1;

QY 2 EASGIGPEVDDRDPEPSIGPVCPFCQCHLRVQCSDGLDKVPRDLPDPTLLDLQNN 61
 DB 32 EASGIGPEVDDRDPEPSIGPVCPFCQCHLRVQCSDGLDKVPRDLPDPTLLDLQNN 86
 QY 62 KITTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLERLYLSKNQKELPERKMPKT 121
 DB 87 KITTEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLERLYLSKNQKELPERKMPKT 146
 QY 122 LOELRAHENEITKRVKVTENGNGNOMIVIELGTNPPLKSSGIENGAFQGMKQLSYIRIADTN 181
 DB 147 LOELRAHENEITKRVKVTENGNGNOMIVIELGTNPPLKSSGIENGAFQGMKQLSYIRIADTN 206
 QY 182 ITSIPQGLPSTLTELHLDGNKISRVDASLKGILNLAQLGSLFNSISAVDNGSLANTPHL 241
 DB 207 ITSIPQGLPSTLTELHLDGNKISRVDASLKGILNLAQLGSLFNSISAVDNGSLANTPHL 266
 QY 242 RELHLDNNKLTTRVPGGLAEHKYIOVVYLLNNNISVVGSSDPFGPHNTKASYSVSLP 301
 DB 267 RELHLDNNKLTTRVPGGLAEHKYIOVVYLLNNNISVVGSSDPFGPHNTKASYSVSLP 326
 QY 302 NPVOYWEIQPSTFRVCVYRSAIQLGNYK 329
 DB 327 NPVOYWEIQPSTFRVCVYRSAIQLGNYK 354

RESULT 4

US-10-319-130-19
 ; Sequence 19, Application US/10319130
 ; Publication No. US20030148351A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Henry, Stephen P
 ; APPLICANT: Mayne, Richard
 ; APPLICANT: Hook, Magnus
 ; TITLE OF INVENTION: NUCLEIC ACID AND PROTEIN SEQUENCES OF ASPORINS
 ; FILE REFERENCE: 12740.0234.NPUS02
 ; CURRENT APPLICATION NUMBER: US/10/319,130
 ; CURRENT FILING DATE: 2002-12-13
 ; PRIOR APPLICATION NUMBER: US 60/341,537
 ; PRIOR FILING DATE: 2001-12-13
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 19
 ; LENGTH: 369
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-319-130-19

Query Match 57.5%; Score 984.5; DB 12; Length 369;
 Best Local Similarity 57.6%; Pred. No. 7.4e-84;
 Matches 190; Conservative 51; Mismatches 86; Indels 3; Gaps 2;

QY 2 EASGIGPE--VPDDRDEPSIGPVCPFCQCHLRVQCSDGLDKVPRDLPDPTLLDLQ 59
 DB 40 EASGIGPE--VPDDRDEPSIGPVCPFCQCHLRVQCSDGLDKVPRDLPDPTLLDLQ 99
 QY 60 NNKITEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLERLYLSKNQKELPERKMP 119
 DB 100 NNKITEIKDGFKNLKNLHLLVNNKISKVSPGAFPLVLERLYLSKNQKELPERKMP 159
 QY 120 KTLQELRAHENEITKRVKVTENGNGNOMIVIELGTNPPLKSSGIENGAFQGMKQLSYIRIAD 179
 DB 160 KTLQELRAHENEITKRVKVTENGNGNOMIVIELGTNPPLKSSGIENGAFQGMKQLSYIRIAD 218


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; Sequence 2, Application US/09866028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION DATA REMOVED - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 2
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-2

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Query Match      55.1%; Score 943.5; DB 9; Length 379;
Best Local Similarity 55.0%; Pred. No. 5,4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

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QY 11 PDRDDEPSLGPVCPFCQCHLRVQCSVDLGLDKVPRDLPDTLLDQNNKITEIKDGD 70
DB 61 PRSHFPFDLPFCPCFCQCHLRVQCSVDLGLDKVPRDLPDTLLDQNNKITEIKEND 120
QY 71 FKLNKLNHALILNNKSKSPGAFPTLVLELYSKNOLKELPEKMPKTLDELRAHEN 130
DB 121 FKELTSLYLGLILNNKLTKEHPAFLLTKKLRLYLSSHNLSEIPLNLPKSLAELRIHEN 180
QY 131 EITKVRKVTENGNNOMIVIELGTPNPKSGIENGAFQMKKLSYIRIADNINISPOGAP 190
DB 181 KVKIKQKDTFKGNALHVLMSANPLDNNGIEFGAFEGV-TVHIRIAKAKLTSVPGKLP 239
QY 191 PSUTLEHLGDNKISRVDASLKGILNMLAKGLSFNSISAVDNGSLANTPHIRELHLDNNK 250
DB 240 PTLLEHLDYNKISTVELDEPKRYKELQRLGIDGNNKTTDIEGNSLANIPRVREIHLNNK 299
QY 251 LTVPGGLAHKTIQVYVLYLNNNISVYSSDFPCPGHNTKKASYGVLSFNFVQWEIQ 310
DB 300 LKKIPSGLPKLTQIIFLHNSNIAVGVNDFPTVPMKKKSLYSALISFNNPKWEMQ 359
QY 311 PSTFRCYVVSATOLGNY 328
DB 360 PATFRCYLSRMSYQLGNF 377

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RESULT 8
US-09-944-449-2
; Sequence 2, Application US/09944449
; Patent No. US20020102647A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary
; APPLICANT: Goddard, Audrey

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; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,449
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: NO. US20020102647A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: NO. US20020102647A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095

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;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 2
;; LENGTH: 379
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-944-449-2
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Query Match 55.1%; Score 943.5; DB 10; Length 379;
Best Local Similarity 55.0%; Pred. No. 5.4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;
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QY 11 PDDRRPESLIGPVCFRCOCHRVQCSDLGDKVPKPLPPTLLDIONNKTEIKXGD 70
DB 61 PRSHFPFDLPFCWCFGCCTSRVHCSDLGTSVPTNIPETRLDIONNKTEIKXND 120
QY 71 FKNLNLHALILVNNKISKVSPGAFTPVKLERLYISKQULKEPEKPKTLOBRAHEN 130
DB 121 FKGLSLVGLILNNKRLKIRHKAPLTTRKLRRLVLSNQSLSEILNPKSLAEIRHEN 180
QY 131 EITKRAKTYFNGLNOMIYIELGTPVKSQGIENGAPQCKSLSYRIADVTNITSIPQGLP 190
DB 181 KVKTKQKOTFKGMNLAHLTEMSANPLDNNGLIEPGAEEGV-TVFHIRIAEAKLTSVPKGLP 239
QY 191 PSLELHLDGNKISIVDASLKGILNNLAKLGISFRSISAVNGSLANTPHRLRLDNNK 250
DB 240 PTLLEHLHDYNKISIVLEDEDFRYEQLRLGIGNKRTIDIEGSLANTPRVHEHLNNK 299
QY 251 LTRVVGGLAEHKYIGVYILHNNNISVVGSSDPCPGHNTKASYSGVSLFSPVQYWEIQ 310
DB 300 LKKTISGLPELKYLOIITLHNSIARVGVNDPCFVPMKKSLSYSAISLFNNPVKTMWQ 359
QY 311 PSTRCVYVRSALIGQNTY 328
DB 360 PATFRCVLSRMSVQLGNF 377
```

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RESULT 9
US-09-944-457-2
; Sequence 2, Application US/09944457
; Patent No. US20020110859A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
```

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;; APPLICANT: Wood, William
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P254BP1C1
;; CURRENT APPLICATION NUMBER: US/09/944,457
;; CURRENT FILING DATE: 2001-09-26
;; PRIOR APPLICATION NUMBER: 09/866,028
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/067,411
;; PRIOR FILING DATE: December 3, 1997
;; PRIOR APPLICATION NUMBER: 60/069,334
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,335
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,278
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,425
;; PRIOR FILING DATE: December 12, 1997
;; PRIOR APPLICATION NUMBER: 60/069,696
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,694
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,702
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,870
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/069,873
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068,017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,082
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,286
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020110859A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
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PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 2
LENGTH: 379
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-457-2

Query Match 55.1%; Score 943.5; DB 10; Length 379;
Best Local Similarity 55.0%; Pred. No. 5.4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDRDEPSPGLGVCPPRCQCHLRVQCSDLGDKVCKDLPPTTLTLDLQNNKITEIKDGD 70
DB 61 PRSHFPDLFPWCPCGCGCYRVCVHSCDLGLTSVPTNIPDTRMDLQNNKIKEIKEND 120
QY 71 FKNLKNLHLLVNNKISKVSPGAFPLVYKLERLYSKQQLKELPKRMPTTLOELRAHEN 130
DB 121 FGLSLSYGLILNNNLTGKHPPAFLLTKKRLRLYLSHQSLSEIPLNLPKSLAEIRIHEN 180
QY 131 BITKVKATPENGNGNOMIVIELGNTPKSGIENGAFQKKKLSYIRIADTNITSIPOGLP 190
DB 181 KYKKIKOKDTFKGNMAHVEMSANPLDNNGIEFGAEGV-TVHIIAEKGLSVKGLP 239
QY 191 PSTELHLDGNKISRVAASLKLANNIAKGLSFNSISAVDNGSLANTPHLEHLDDNK 250
DB 240 PTLLEHLNKNISTYLEDEPKRYKELQRLGLGNNTITDIENGSLNIPRVREIHLNNK 299
QY 251 LRRVPGLAHKKIQVYVLLHNNNISVYGSDFCPPHGNTKKASYSVSLPSNVQYWEIQ 310
DB 300 LKKIPGGLPELKYLIQIFLHNSIARVGVDFCTVPKMKKSLYSALSFPNNVKYWEIQ 359
QY 311 PSTFRCVYVSATOLGNY 328
DB 360 PATFRCVLSRMSVQLGNF 377

RESULT 10
US-09-944-862-2
Sequence 2, Application US/09944862
Patent No. US20020115145A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerltsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Guiney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944, 862
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866, 028
PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/067, 411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069, 334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069, 696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068, 017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070, 440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074, 086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074, 092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075, 945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112, 850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113, 296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146, 222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216, 021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218, 517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254, 311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020115145A1, December 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020115145A1, December 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520

;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 2
;; LENGTH: 379
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-944-862-2

Query Match 55.1%; Score 943.5; DB 10; Length 379;
Best Local Similarity 55.0%; Pred. No. 5.4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDRDPEPSLGPVCPRCQCHLVVQCSDLGLKVPKDLPPDTTLDLNNKITEIKGD 70
DB 61 PRSHFPFDFPWCPCQCCYSRVVCSDDLTSVPINIPFDRMDLQNNKIKEIKEND 120
QY 71 FKVLKMLHLILNNKISKPSGAFPLVLELYLSKNDKELPEKMTLOELAHEN 130
DB 121 FKGLTSLYGLILNNKLTTHPAFLTTKRLRLYLSHQLSBIPLNLPKSLAELRIHEN 180
QY 131 EITKRVKTVENGILNOMIVIELGNPLKSGIENGAFQMKKLSYIRIADNTNITSIFQGLP 190
DB 181 KYVKIKQDFTFKGNALHVLSEMSANPLDNGIEFGAFEGV-TVPHIRIAEAKLTSVEKGLP 239
QY 191 PSLTEHLDNKISRVDASLKLNLNLAKGLSFNSISAVDNGSLANTPHRLAHLDNKK 250
DB 240 PTLLEHLIDYNNKISTVELEDFKRYKELQRLGLNNKTIENGSLANIPRREIHLNKK 299
QY 251 LRRVPGSLMEKHTIQVYVILNNNISVVGSSDFCPRGNTKASGVSLFSNVQWEIO 310
DB 300 LKKIPGSLPELKLQIIFLHSNSIARVANDFCPTVPMKKSLYSASLFFNNPVKWEIO 359
QY 311 PSTFCVYVSATQIGNY 328
DB 360 PATFRCVLSHMSYQLGNF 377

RESULT 11
US-09-945-587-2
; Sequence 2, Application US/09945587
; Patent No. US20020127643A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Batton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,587
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997

;; PRIOR APPLICATION NUMBER: 60/069,425
;; PRIOR FILING DATE: December 12, 1997
;; PRIOR APPLICATION NUMBER: 60/069,696
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,694
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,702
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,870
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/069,873
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068,017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020127643A1member 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020127643A1member 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; SEQ ID NO 2
;; LENGTH: 379
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-945-587-2

Query Match 55.1%; Score 943.5; DB 10; Length 379;
Best Local Similarity 55.0%; Pred. No. 5.4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

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QY 11 PDDRPEPSLGVPCPCQCHLRVYCCSDGLDVKVPKDLPPDTLLDQNNKITEIKGD 70
DB 61 PRSHFPFPLFMCPFGCCYRVHCSDLGLTSVPTNIPDTMLDQNNKITEIKEND 120
QY 71 FNLKLNHALLVNNKISRVSPGAFPLVLEKLYLSKNQOLKEPEKPKTLQELRAHEN 130
DB 121 FKGTLSTVLGLINNNKLTIRPKAFITTKLRRLVLSHQBLEIPNLKSLAEIRIHEN 180
QY 131 ETTKRTKTFNGLNOMIVLELTNPVKSQSGIENGAFQCKKLSYRIADTNTISIPQGLP 190
DB 161 KVKKIQKQTFKGMALHVLKMSANPLDNNGIEPGAEGV-TVPHIRIAEAKLTSVPGKLP 239
QY 191 PSLTSLHLDGKNSIRSDASLKGNNLAKLGSFNSISAVNDGSLANPHLEHLDDNNK 250
DB 240 PTLLEHLDDYKNTIWELEDFFKRYKELQRLGKNNKTIIDENGSLANIPREIHLNNK 299
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DB 300 LKKIRSGLPKLYLQIFLHNSIARVGVNDFCPTVPKMKSLYSALISFNNPVKYMENQ 359
QY 311 PSTFCYVRSALQICNY 328
DB 360 PATFCVLSRMSVOLGNF 377
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RESULT 12

US-09-945-015-2

/ Sequence 2, Application US/09945015
/ Patent No. US20020132768A1

/ GENERAL INFORMATION:

/ APPLICANT: Baker, Kevin

/ APPLICANT: Botstein, David

/ APPLICANT: Eaton, Dan

/ APPLICANT: Ferrara, Napoleone

/ APPLICANT: Filvaroff, Ellen

/ APPLICANT: Gerritsen, Mary

/ APPLICANT: Goddard, Audrey

/ APPLICANT: Godowski, Paul

/ APPLICANT: Grimaldi, Christopher

/ APPLICANT: Gurney, Austin

/ APPLICANT: Hillan, Kenneth

/ APPLICANT: Kijavlin, Ivar

/ APPLICANT: Napier, Mary

/ APPLICANT: Roy, Margaret

/ APPLICANT: Tumas, Daniel

/ APPLICANT: Wood, William

/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

/ FILE REFERENCE: P2548P1C1

/ CURRENT APPLICATION NUMBER: US/09/945,015

/ PRIOR FILING DATE: 2001-09-26

/ PRIOR APPLICATION NUMBER: 09/866,028

/ PRIOR FILING DATE: 2001-05-25

/ PRIOR APPLICATION NUMBER: 60/067,411

/ PRIOR FILING DATE: December 3, 1997

/ PRIOR APPLICATION NUMBER: 60/069,334

/ PRIOR FILING DATE: December 11, 1997

/ PRIOR APPLICATION NUMBER: 60/069,335

/ PRIOR FILING DATE: December 11, 1997

/ PRIOR APPLICATION NUMBER: 60/069,278

/ PRIOR FILING DATE: December 11, 1997

/ PRIOR APPLICATION NUMBER: 60/069,425

/ PRIOR FILING DATE: December 12, 1997

/ PRIOR APPLICATION NUMBER: 60/069,696

/ PRIOR FILING DATE: December 16, 1997

/ PRIOR APPLICATION NUMBER: 60/069,694

/ PRIOR FILING DATE: December 16, 1997

/ PRIOR APPLICATION NUMBER: 60/069,702

/ PRIOR FILING DATE: December 16, 1997

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/ PRIOR APPLICATION NUMBER: 60/069,870
/ PRIOR FILING DATE: December 17, 1997
/ PRIOR APPLICATION NUMBER: 60/069,873
/ PRIOR FILING DATE: December 17, 1997
/ PRIOR APPLICATION NUMBER: 60/068,017
/ PRIOR FILING DATE: December 18, 1997
/ PRIOR APPLICATION NUMBER: 60/070,440
/ PRIOR FILING DATE: January 5, 1998
/ PRIOR APPLICATION NUMBER: 60/074,086
/ PRIOR FILING DATE: February 9, 1998
/ PRIOR APPLICATION NUMBER: 60/074,092
/ PRIOR FILING DATE: February 9, 1998
/ PRIOR APPLICATION NUMBER: 60/075,945
/ PRIOR FILING DATE: February 25, 1998
/ PRIOR APPLICATION NUMBER: 60/112,850
/ PRIOR FILING DATE: December 16, 1998
/ PRIOR APPLICATION NUMBER: 60/113,296
/ PRIOR FILING DATE: December 22, 1998
/ PRIOR APPLICATION NUMBER: 60/146,222
/ PRIOR FILING DATE: July 28, 1999
/ PRIOR APPLICATION NUMBER: PCT/US98/19330
/ PRIOR FILING DATE: September 15, 1998
/ PRIOR APPLICATION NUMBER: PCT/US98/25108
/ PRIOR FILING DATE: December 1, 1998
/ PRIOR APPLICATION NUMBER: 09/216,021
/ PRIOR FILING DATE: December 16, 1998
/ PRIOR APPLICATION NUMBER: 09/218,517
/ PRIOR FILING DATE: December 22, 1998
/ PRIOR APPLICATION NUMBER: 09/254,311
/ PRIOR FILING DATE: March 3, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/12252
/ PRIOR FILING DATE: June 22, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/21090
/ PRIOR FILING DATE: September 15, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/28409
/ PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/28313
/ PRIOR FILING DATE: No. US20020132768A1ember 30, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/28301
/ PRIOR FILING DATE: December 1, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/30095
/ PRIOR FILING DATE: December 16, 1999
/ PRIOR APPLICATION NUMBER: PCT/US00/03565
/ PRIOR FILING DATE: February 11, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/04414
/ PRIOR FILING DATE: February 22, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/05841
/ PRIOR FILING DATE: March 2, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/08439
/ PRIOR FILING DATE: March 30, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/14042
/ PRIOR FILING DATE: May 22, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/20710
/ PRIOR FILING DATE: July 28, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/32678
/ PRIOR FILING DATE: December 1, 2000
/ PRIOR APPLICATION NUMBER: PCT/US01/06520
/ PRIOR FILING DATE: February 28, 2001
/ NUMBER OF SEQ ID NOS: 120
/ SEQ ID NO 2
/ LENGTH: 379
/ TYPE: PRT
/ ORGANISM: Homo Sapien
/ US-09-945-015-2
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Query Match 55.1%; Score 943.5; DB 10; Length 379;
Best Local Similarity 55.0%; Pred. No. 5.4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

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QY 11 PDDDRPEPSLGVPCPCQCHLRVYCCSDGLDVKVPKDLPPDTLLDQNNKITEIKGD 70
DB 61 PRSHFPFPLFMCPFGCCYRVHCSDLGLTSVPTNIPDTMLDQNNKITEIKEND 120
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Qy 71 FKNLKNLHALLLVNKKSKVSPGAFPLVVKLERLYLSKNQKELPEKMPKTLQELRAHEN 130
Db 121 FKGLTSLVGLLNNKLTKEHPKAFLLTKLRRLYLSNQSSEIPLNPKSLAEIRIHEN 180
Qy 131 EITVRKVTENGLOMITYIELGTNPLKSSGIENGAFQGMKLSYRIRADNITSIPQGLP 190
Db 181 KVKKIQTQTFKGMNALHLEWISANPLDNGIEPGAPEGV-TVFHRIAEAKLTVPKGLP 239
Qy 191 PSTLHLDGNKISRVDAASLKGILNLAKEISFNSIAVDNGSLANTPHLREHLDNK 250
Db 240 FTLEHLDHYNKISVLEJEDFRKYELORLGGNNKIDIERGSLANIPRAHEHLENNK 299
Qy 251 LTRVPGIAEKKYIQVYVLAHNNISVSGSDPCPGHNTKKAASVGSVLSFNSPVQWIEQ 310
Db 300 LKKIIPSGIPELKKYQIIFLHNSISARVGVNDFCTVPKMKSLYSALSIFNNPVKXWEMQ 359
Qy 311 PSTRCYVVRSAIQGNV 328
Db 360 PATFRCVLSRMSVOLGNF 377

RESULT 13.
US-09-944-396-2
Sequence 2, Application US/09944396
Patent No. US20020132981A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Batson, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Guiney, Aubeth
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548PCL
CURRENT APPLICATION NUMBER: US/09/944,396
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998

PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020132981A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020132981A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
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PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 2
LENGTH: 379
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-396-2

Query Match 55.1%; Score 943.5; DB 10; Length 379;
Best Local Similarity 55.0%; Pred. No. 5.4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

Qy 11 PDDDBFBSLGPVCPFCQCLARVQCSDGLDVKVPKOLPDDTLDDIKNKKTITKXGD 70
Db 61 PRSHFPFPLDFPWCFFGQCYSRVHCSDLGLTSVPTNIPDTRMLDQNNKIKEIKEND 120
Qy 71 FKNLKNLHALLLVNKKSKVSPGAFPLVVKLERLYLSKNQKELPEKMPKTLQELRAHEN 130
Db 121 FKGLTSLVGLLNNKLTKEHPKAFLLTKLRRLYLSNQSSEIPLNPKSLAEIRIHEN 180
Qy 131 EITVRKVTENGLOMITYIELGTNPLKSSGIENGAFQGMKLSYRIRADNITSIPQGLP 190
Db 181 KVKKIQTQTFKGMNALHLEWISANPLDNGIEPGAPEGV-TVFHRIAEAKLTVPKGLP 239

APPLICANT: Baker, Kevin
 APPLICANT: Botstein, David
 APPLICANT: Batson, Dan
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gerritsen, Mary
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul
 APPLICANT: Grimaldi, Christopher
 APPLICANT: Gueney, Austin
 APPLICANT: Hillan, Kenneth
 APPLICANT: Kijavlin, Ivar
 APPLICANT: Napier, Mary
 APPLICANT: Roy, Margaret
 APPLICANT: Tomas, Daniel
 APPLICANT: Wood, William
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P2548P1C1
 CURRENT APPLICATION NUMBER: US/09/943,762
 PRIOR FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: 09/866,028
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/067,411
 PRIOR FILING DATE: December 3, 1997
 PRIOR APPLICATION NUMBER: 60/069,334
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,335
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,278
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,425
 PRIOR FILING DATE: December 12, 1997
 PRIOR APPLICATION NUMBER: 60/069,696
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,694
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,702
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,870
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/069,873
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/068,017
 PRIOR FILING DATE: December 18, 1997
 PRIOR APPLICATION NUMBER: 60/070,440
 PRIOR FILING DATE: January 5, 1998
 PRIOR APPLICATION NUMBER: 60/074,086
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/074,092
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/075,945
 PRIOR FILING DATE: February 25, 1998
 PRIOR APPLICATION NUMBER: 60/112,850
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 60/113,296
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 60/146,222
 PRIOR FILING DATE: July 28, 1999
 PRIOR APPLICATION NUMBER: PCT/US98/19330
 PRIOR FILING DATE: September 16, 1998
 PRIOR APPLICATION NUMBER: PCT/US98/25108
 PRIOR FILING DATE: December 1, 1998
 PRIOR APPLICATION NUMBER: 09/216,021
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 09/218,517
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 09/254,311
 PRIOR FILING DATE: March 3, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/12252
 PRIOR FILING DATE: June 22, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: September 15, 1999

PRIOR APPLICATION NUMBER: PCT/US99/28409
 PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28313
 PRIOR FILING DATE: No. US20020142958A1ember 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28301
 PRIOR FILING DATE: December 1, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/30095
 PRIOR FILING DATE: December 16, 1999
 PRIOR APPLICATION NUMBER: PCT/US00/03565
 PRIOR FILING DATE: February 11, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: February 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/05841
 PRIOR FILING DATE: March 2, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/08439
 PRIOR FILING DATE: March 30, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/14042
 PRIOR FILING DATE: May 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/20710
 PRIOR FILING DATE: July 28, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/32678
 PRIOR FILING DATE: December 1, 2000
 PRIOR APPLICATION NUMBER: PCT/US01/06520
 PRIOR FILING DATE: February 28, 2001
 NUMBER OF SEQ ID NOS: 120
 SEQ ID NO 2
 LENGTH: 379
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-09-943-762-2

Query Match 55.1%; Score 943.5; DB 10; Length 379;
 Best Local Similarity 55.0%; Pred. No. 5.4e-80;
 Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDRFESLGPVCEPCQCHLRVQCSDLGLDKVPKDLPPDTLLDLQNNKITEIKGD 70
 DB 61 PRSHFPFDLPFMCFCGQCYSRVHGSGLGTSTPTNIPTDRLDLQNNKIKIKEND 120
 QY 71 FKNLKNLHALLVNNKISKVSPGAFPTLVKLERLYLSNQKELPEKPKTLQELRAHN 130
 DB 121 FKGTLSTLYGLILNNKIKKIHKPAFLTTKGLRRRLYSNQLSEIPLNPKSLAEIRIHEN 180
 QY 131 EITKVRKVTFGNLMQVTELTGTNPLKSSGTENGAFQGMKGLSYRIADTNTSIPQGLP 190
 DB 131 KYKIKQKTFKGMALHVLKSNANPLDNGGLEPQAFSEV-TVFHRIKAEKLTSPKGLP 239
 QY 191 PSLTEHLIDGNKISRVAASLKGILNLAQGLSFNSISAVDNGSLANTPHLREHLIDNNK 250
 DB 240 PTLLEHLIDYNNKISTVELDEPKRYKXELQRLGLGNKKITDIENGSLANTPRVREIHLNNK 299
 QY 251 LTRVPGSLAEKTYIQVYVILHNNNISVVGSSDPFCPPGANTKASISGUSLPSNPQVYWEIO 310
 DB 300 LKIKPSGLPELKYIQLITFLHNSIARVGVNDPCTVPMKKSILYSALISLFNNPVKYMEO 359
 QY 311 PSTFRCVVRSAIOIGNY 328
 DB 360 PATFRCVLSRMSVQDGNP 377

RESULT 17
 US-09-944-654-2
 Sequence 2, Application US/09944654
 Patent No. US20020142959A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Botstein, David
 APPLICANT: Batson, Dan
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gerritsen, Mary
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul

APPLICANT: Grimaldi, Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Hillan, Kenneth
 APPLICANT: Kijaviri, Ivar
 APPLICANT: Napier, Mary
 APPLICANT: Roy, Margaret
 APPLICANT: Tumas, Daniel
 APPLICANT: Wood, William
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P2548P1C1
 CURRENT APPLICATION NUMBER: US/09/944,654
 CURRENT FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: 60/866,028
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/067,411
 PRIOR FILING DATE: December 3, 1997
 PRIOR APPLICATION NUMBER: 60/069,334
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,335
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,278
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,425
 PRIOR FILING DATE: December 12, 1997
 PRIOR APPLICATION NUMBER: 60/069,696
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,694
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,702
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,870
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/069,873
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/068,017
 PRIOR FILING DATE: December 18, 1997
 PRIOR APPLICATION NUMBER: 60/070,440
 PRIOR FILING DATE: January 5, 1998
 PRIOR APPLICATION NUMBER: 60/074,086
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/074,092
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/075,945
 PRIOR FILING DATE: February 25, 1998
 PRIOR APPLICATION NUMBER: 60/112,850
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 60/113,296
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 60/146,222
 PRIOR FILING DATE: July 28, 1999
 PRIOR APPLICATION NUMBER: PCT/US98/19330
 PRIOR FILING DATE: September 16, 1998
 PRIOR APPLICATION NUMBER: PCT/US98/25108
 PRIOR FILING DATE: December 1, 1998
 PRIOR APPLICATION NUMBER: 09/216,021
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 09/218,517
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 09/254,311
 PRIOR FILING DATE: March 3, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/12252
 PRIOR FILING DATE: June 22, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: September 15, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28409
 PRIOR FILING DATE: NO. US20020142959A1ember 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28313
 PRIOR FILING DATE: NO. US20020142959A1ember 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28301
 PRIOR FILING DATE: December 1, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/30095
 PRIOR FILING DATE: December 16, 1999

PRIOR APPLICATION NUMBER: PCT/US00/03565
 PRIOR FILING DATE: February 11, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: February 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/05841
 PRIOR FILING DATE: March 2, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/08439
 PRIOR FILING DATE: March 30, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/14042
 PRIOR FILING DATE: May 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/20710
 PRIOR FILING DATE: July 28, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/32678
 PRIOR FILING DATE: December 1, 2000
 PRIOR APPLICATION NUMBER: PCT/US01/06520
 PRIOR FILING DATE: February 28, 2001
 NUMBER OF SEQ ID NOS: 120
 SEQ ID NO 2
 LENGTH: 379
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-09-944-654-2
 Query Match 55.1%; Score 943.5; DB 10; Length 379;
 Best Local Similarity 55.0%; Pred. No. 5.4e-80;
 Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;
 11 PDDRRFEESLSIPVCGFCRCHLRVQCGSDLGIDKVPKLPDPTLLD:ONNKITEIKOSD 70
 61 PSHFFPPDLFPWCFCGQCYSRVHCSDLGITVTPITPDTRLMD:ONNKIKKIKEND 120
 71 FENLKNLHALLIVNNKISKVSPGAFPTPLVKLERLYSKNOUKELPEKMPKTLQSDRAHEN 130
 121 FKGLTSLXGLIANNKCLKIKPKAFLLTKCLRLYLSTNQLSEITLNP:PKSLAEIRIHEN 180
 131 EITVRKVTENGALNOMIVIEIETNPELKSSEIENGAFQGMKKLSYRIADNTITS:IPQGLP 190
 181 KYKIKQKOTPKGMNLAHLBMSANPLDNNNGIEPGAFBEV-TVFHIRIAEAKLTSVPKGLP 239
 191 PSUTLHLDKDKISVYDAASLKGMLNKLKLGISFISIAVNDGSLANTPHLRRLHLDDNK 250
 240 PLLLEHLDYKISVLEDEDFRKYKEIQRLGIGNNKIIDINGSLANT:PRVEIHLLENKK 299
 251 LTRVPGIAEAKYQOVVLIHNNNISVVGSDPCPPGHNTKKAASVGSLSFNPVOYWEIQ 310
 300 LKKTSPGPELKTILOITILHNSIARVGVNDPCFVPPKKSLSYSAISLFNNPVKTEMQ 359
 311 PSTFRCVYVRSALQKYN 328
 360 PATFRCVLSRMSVQGNF 377
 Db
 RESULT 18
 US-09-943-851A-2
 Sequence 2, Application US/09943851A
 Patent No. US20020150976A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Botstein, David
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gerritsen, Mary
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul
 APPLICANT: Grimaldi, Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Hillan, Kenneth
 APPLICANT: Kijaviri, Ivar
 APPLICANT: Napier, Mary
 APPLICANT: Roy, Margaret
 APPLICANT: Tumas, Daniel
 APPLICANT: Wood, William

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548PICI
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US/09/943, 851A
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US/09/866, 028
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069, 334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069, 696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068, 017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070, 440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074, 086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074, 092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075, 945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112, 850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113, 296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146, 222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216, 021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218, 517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254, 311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020150976A1member 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020150976A1member 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000

PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 2
LENGTH: 379
TYPE: PRT
ORGANISM: Homo Sapien
US-09-943-851A-2
Query Match 55.1%; Score 943.5; DB 10; Length 379;
Best Local Similarity 55.0%; Pred. No. 5.4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;
QY 11 PDDRPEPSIGPVCPFCQCHLRVQCSDLGDKVPEKDIAPPDTLLDLQNNKITEIKQD 70
DB 61 PRSHFPFDLPFCPCGCGCYSRVVACSDGLTSVPTNIPTDRMLDLQNNKIKEIKEND 120
QY 71 FKRLKTLALILVNNKISKVSFGAFLPYLKERLYISKQQLKELPKMKPTLOELPAHEN 130
DB 121 FKLGLTSLYGLILNNNDLTTHIPKAFLTTKRLRLYLSHQLSSEIPLNPKSLAEIRIHEN 180
QY 131 EITKVKVTEFNGINOMIVLELTGTPKSSGIENGAFQGGKKSITRIADTNITISPOGR 190
DB 181 KKKKIOKOTFKKNNALHTEMANPLDNNNGIEPGEAGV-TVPHIIEKKLTVKGLP 239
QY 191 PSITELHLDGNTKSRVDAASLXGLNNLAVLGISFNISAVDNGSLANTPHLEHLDNNK 250
DB 240 FTLLEHLIDYNNKISTVELDPKRYKELQRLGNNKITIDENGSLANIRVREIHLENNK 299
QY 251 LRVPGGLAEKTYIQVYVYHNNNISVYSSDPCPEGHTTKKASVCSVLSFSPVQYWEIO 310
DB 300 LKKIPGELPELKYLOIIFLHNSNISARVGVNDFCPVKKKKLSYSAISIFNNPVKYMWO 359
QY 311 PSTPRCVYRSALIOGNY 328
DB 360 PATFRCVLSRMSVQJGNF 377
RESULT 19
US-09-944-413-2
Sequence 2, Application US/09944413
Patent No. US2002015604A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gottlieb, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Gimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavini, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548PICI
CURRENT APPLICATION NUMBER: US/09/944, 413
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866, 028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067, 411

PRIOR	FILING DATE:	December 3, 1997	
PRIOR	APPLICATION NUMBER:	60/069,334	
PRIOR	FILING DATE:	December 11, 1997	
PRIOR	APPLICATION NUMBER:	60/069335	
PRIOR	FILING DATE:	December 11, 1997	
PRIOR	APPLICATION NUMBER:	60/069,278	
PRIOR	FILING DATE:	December 11, 1997	
PRIOR	APPLICATION NUMBER:	60/069,425	
PRIOR	FILING DATE:	December 12, 1997	
PRIOR	APPLICATION NUMBER:	60/069,696	
PRIOR	FILING DATE:	December 16, 1997	
PRIOR	APPLICATION NUMBER:	60/069,694	
PRIOR	FILING DATE:	December 16, 1997	
PRIOR	APPLICATION NUMBER:	60/069,702	
PRIOR	FILING DATE:	December 16, 1997	
PRIOR	APPLICATION NUMBER:	60/069,870	
PRIOR	FILING DATE:	December 17, 1997	
PRIOR	APPLICATION NUMBER:	60/069,873	
PRIOR	FILING DATE:	December 17, 1997	
PRIOR	APPLICATION NUMBER:	60/068,017	
PRIOR	FILING DATE:	December 18, 1997	
PRIOR	APPLICATION NUMBER:	60/070,440	
PRIOR	FILING DATE:	January 5, 1998	
PRIOR	APPLICATION NUMBER:	60/074,086	
PRIOR	FILING DATE:	February 9, 1998	
PRIOR	APPLICATION NUMBER:	60/074,092	
PRIOR	FILING DATE:	February 9, 1998	
PRIOR	APPLICATION NUMBER:	60/075,945	
PRIOR	FILING DATE:	February 25, 1998	
PRIOR	APPLICATION NUMBER:	60/112,850	
PRIOR	FILING DATE:	December 16, 1998	
PRIOR	APPLICATION NUMBER:	60/113,296	
PRIOR	FILING DATE:	December 22, 1998	
PRIOR	APPLICATION NUMBER:	60/146,222	
PRIOR	FILING DATE:	July 28, 1999	
PRIOR	APPLICATION NUMBER:	PCT/US98/19330	
PRIOR	FILING DATE:	September 16, 1998	
PRIOR	APPLICATION NUMBER:	PCT/US98/25108	
PRIOR	FILING DATE:	December 1, 1998	
PRIOR	APPLICATION NUMBER:	09/216,021	
PRIOR	FILING DATE:	December 16, 1998	
PRIOR	APPLICATION NUMBER:	09/218,517	
PRIOR	FILING DATE:	December 22, 1998	
PRIOR	APPLICATION NUMBER:	09/254,311	
PRIOR	FILING DATE:	March 3, 1999	
PRIOR	APPLICATION NUMBER:	PCT/US99/12252	
PRIOR	FILING DATE:	June 22, 1999	
PRIOR	APPLICATION NUMBER:	PCT/US99/21090	
PRIOR	FILING DATE:	September 15, 1999	
PRIOR	APPLICATION NUMBER:	PCT/US99/28409	
PRIOR	FILING DATE:	No. US20020156094A	amber 30, 1999
PRIOR	APPLICATION NUMBER:	PCT/US99/28313	
PRIOR	FILING DATE:	No. US20020156094A	amber 30, 1999
PRIOR	APPLICATION NUMBER:	PCT/US99/28301	
PRIOR	FILING DATE:	December 1, 1999	
PRIOR	APPLICATION NUMBER:	PCT/US99/30095	
PRIOR	FILING DATE:	December 16, 1999	
PRIOR	APPLICATION NUMBER:	PCT/US00/03565	
PRIOR	FILING DATE:	February 11, 2000	
PRIOR	APPLICATION NUMBER:	PCT/US00/04414	
PRIOR	FILING DATE:	February 22, 2000	
PRIOR	APPLICATION NUMBER:	PCT/US00/05841	
PRIOR	FILING DATE:	March 2, 2000	
PRIOR	APPLICATION NUMBER:	PCT/US00/08439	
PRIOR	FILING DATE:	March 30, 2000	
PRIOR	APPLICATION NUMBER:	PCT/US00/14042	
PRIOR	FILING DATE:	May 22, 2000	
PRIOR	APPLICATION NUMBER:	PCT/US00/20710	
PRIOR	FILING DATE:	July 26, 2000	
PRIOR	APPLICATION NUMBER:	PCT/US00/32678	
PRIOR	FILING DATE:	December 1, 2000	
PRIOR	APPLICATION NUMBER:	PCT/US01/06520	
PRIOR	FILING DATE:	February 28, 2001	

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? NUMBER OF SEQ ID NOS: 120
? SEQ ID NO 2
? LENGTH: 379
? TYPE: PRT
? ORGANISM: Homo Sapien
US-09-944-413-2

Query Match      55.1%; Score 943.5; DB 10; Length 379;
Best Local Similarity .55.0%; Pred. No. 5.4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

Oy      11 PDDDFSPSPGVPVPCQCHLRVQCSDDLGVPPDLPDPTLLDLONNKITEIKDGD 70
Db      61 PRGFFPFDPFPCPCFCCQCYSRVHCSDDLGLTSVPFNIPDITMDLONNKIKEIKEND 120
Oy      71 FKNLKNLHALILVNNKISKVSPGAFPLVYLERLYLSKNOLKELPERKPKTLQELRAHEN 130
Db      121 FKGLTSLYGLIILNNKTLKTHPKAFLLTKKLRLYLSHNOQSEIRPLMKSLAEIRIHEN 180
Oy      131 EITVKRVKVTNGLNQMTIVIELGNPLKSGIENGAFQMKKLSTIRLADNTITSIPQGLP 190
Db      181 KKVKIQDQTFPGMAALHVLKESANPLDNNGIEPAPFEGVTVFIRIRIAEAKLTSVPKGLP 239
Oy      191 PSTLEHLDDNKISRVAASLKGILNNLAKIGLSPNSISAVDNGSLANTPHRLHLDDNNK 250
Db      240 PTLLEHLDDNKISTVELEDFKRYKELQRLGLGNKKITDLENGSLANPVRRETHLENNK 299
Oy      251 LTRVPGGLAEHKYIQVAVYLVHNNNISVYGSSDFCPGHNTKASYSGVSLFSPNVOYWEIQ 310
Db      300 LKKIPSGLPHELKYLQIIFLHNSNLSIARGVANDFCPTVRKMKSLYSALSFNNPKYWEHQ 359
Oy      311 PSTFRCYVRSALDGLANY 328
Db      360 PATERCVLSRMSVQLGNF 377

RESULT 20
US-09-944-403-2
? Sequence 2, Application US/09944403
? Patent No. US20020165143A1
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin
? APPLICANT: Botstein, David
? APPLICANT: Baton, Dan
? APPLICANT: Ferrara, Napoleone
? APPLICANT: Filvaroff, Ellen
? APPLICANT: Gerritsen, Mary
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul
? APPLICANT: Grimaldi, Christopher
? APPLICANT: Gurney, Austen
? APPLICANT: Hillan, Kenneth
? APPLICANT: Kijavich, Ivar
? APPLICANT: Napier, Mary
? APPLICANT: Roy, Margaret
? APPLICANT: Tumas, Daniel
? APPLICANT: Wood, William
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? TITLE OF INVENTION: ACIDS ENCODING THE SAME
? FILE REFERENCE: P25481C1
? CURRENT APPLICATION NUMBER: US/09/944,403
? CURRENT FILING DATE: 2001-09-26
? PRIOR APPLICATION NUMBER: 09/866,028
? PRIOR FILING DATE: 2001-05-25
? PRIOR APPLICATION NUMBER: 60/067,411
? PRIOR FILING DATE: December 3, 1997
? PRIOR APPLICATION NUMBER: 60/069,334
? PRIOR FILING DATE: December 11, 1997
? PRIOR APPLICATION NUMBER: 60/069,335
? PRIOR FILING DATE: December 11, 1997
? PRIOR APPLICATION NUMBER: 60/069,278
? PRIOR FILING DATE: December 11, 1997
? PRIOR APPLICATION NUMBER: 60/069,425

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PRIOR FILING DATE: December 12, 1997
 PRIOR APPLICATION NUMBER: 60/069,696
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,694
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,702
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,870
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/069,873
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/068,017
 PRIOR FILING DATE: December 18, 1997
 PRIOR APPLICATION NUMBER: 60/070,440
 PRIOR FILING DATE: January 5, 1998
 PRIOR APPLICATION NUMBER: 60/074,086
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/074,092
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/075,945
 PRIOR FILING DATE: February 25, 1998
 PRIOR APPLICATION NUMBER: 60/112,850
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 60/113,296
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 60/146,222
 PRIOR FILING DATE: July 28, 1999
 PRIOR APPLICATION NUMBER: PCT/US98/19330
 PRIOR FILING DATE: September 16, 1998
 PRIOR APPLICATION NUMBER: PCT/US98/25108
 PRIOR FILING DATE: December 1, 1998
 PRIOR APPLICATION NUMBER: 09/216,021
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 09/218,517
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 09/254,311
 PRIOR FILING DATE: March 3, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/12252
 PRIOR FILING DATE: June 22, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: September 15, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28409
 PRIOR FILING DATE: No. US200201651431member 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28313
 PRIOR FILING DATE: No. US200201651431member 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28301
 PRIOR FILING DATE: December 1, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/30095
 PRIOR FILING DATE: December 16, 1999
 PRIOR APPLICATION NUMBER: PCT/US00/03565
 PRIOR FILING DATE: February 11, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: February 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/05841
 PRIOR FILING DATE: March 2, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/08439
 PRIOR FILING DATE: March 30, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/14042
 PRIOR FILING DATE: May 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/20710
 PRIOR FILING DATE: July 28, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/32678
 PRIOR FILING DATE: December 1, 2000
 PRIOR APPLICATION NUMBER: PCT/US01/06520
 PRIOR FILING DATE: February 28, 2001
 NUMBER OF SEQ ID NOS: 120
 SEQ ID NO 2
 LENGTH: 379
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-09-944-403-2
 Query Match 55.1%; Score 943.5; DB 10; Length 379;

Best Local Similarity 55.0%; Pred. No. 5.4e-80;
 Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;
 QY 11 PDDRFEPSLGPVCFRCQCHLRVQCSDLGDKPKOLPPTTLDDLNKITEIKXD 70
 Db 61 PSHFFPEDLPWCPCQCSRVVHCSDLGLTSPVPMIPPTNMLDNNKIKIKEND 120
 QY 71 FNLKRLHALILVNNKISKVSPGAFPLVTERLYISKQKLEPEKPKTLOEIRAHEN 130
 Db 121 FKLGLSVGLILNNKRLKIKHPKALITTKGLRRLVLSHNSQLEIRANPKSLAEIRIHEN 180
 QY 131 EITVRYKVTENGLOMIVIELGTNPLKSSGIEBNGAPQGNKLSYRIADNTITSIPQGLP 190
 Db 181 KVKKIOKDTFKGMNALHYLEMSANPLDNNGIEPGAFEGV-TVFHIRIAKLTSPKGLP 239
 QY 191 PELTEHLHDNKSISVDASLKGANLAKLGISFISISAVNGSLANTPLHELHDNNK 250
 Db 240 PTLLEHLHDNKSISVLEDFPKRYKELRLGNNKIDTIDENGSLANTPVEIHLENNK 299
 QY 251 LTRVFGSLAEHYIOVVYLHNNNISVGSDFCPGHNTKSKASYSVSLFSNPVOYWEIO 310
 Db 300 LKKISGELPELKYIQTITLHNSISIRVGVNDPCFTVPKKKSLYSALISFNNPKYWEIO 359
 QY 311 PSTFRGVYVRSALIQENTY 328
 Db 360 PATFRGVLSRMSVQLGNF 377
 RESULT 21
 US-09-944-896-2
 Sequence No. 2, Application US/09944896
 Patent No. US20020168715A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Botstein, David
 APPLICANT: Baton, Dan
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gerlstein, Mary
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul
 APPLICANT: Grimaldi, Christopher
 APPLICANT: Gueney, Austlin
 APPLICANT: Hillan, Kenneth
 APPLICANT: Kijavlin, Ivar
 APPLICANT: Napier, Mary
 APPLICANT: Roy, Margaret
 APPLICANT: Tomas, Daniel
 APPLICANT: Wood, William
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P2548P1C1
 CURRENT APPLICATION NUMBER: US/09/944.896
 PRIOR FILING DATE: 2001-08-31
 PRIOR APPLICATION NUMBER: 09/866,028
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/069,334
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069335
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,278
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,425
 PRIOR FILING DATE: December 12, 1997
 PRIOR APPLICATION NUMBER: 60/069,696
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,694
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,702
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,870
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/069,873

```

PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020168715A,ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020168715A,ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 2
LENGTH: 379
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-896-2

```

```

Query Match 55.1%; Score 943.5; DB 10; length 379;
Best Local Similarity 55.0%; Pred. No. 5,4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

```

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QY 11 PDDRDEPSLGPVPCRCCHLVVOCSDLGDKVPEKDLPPDTTLLDQNNKITEIKDQ 70
DB 61 PSHHPFPLDFPCPCGCCGCSYVAVCSGDLGTSVTNPDPTRMDLQNNKIKELKEND 120
QY 71 FKNLKNLHLLVNNKISKVSPPAFPLVLELYLSKQKELPERMPTLOELPAHEN 130
DB 121 FKGLTSLYGLILNNKLTYSKHPAFPLTTKRLRLYLSHQLSSEIPLNLPKSLAEIRIHEN 180

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QY 131 EITKRVKTFNGLNOMIVIELGTNPLKSSGIEGAFQMKLSYIRIADNTITSIPQGLP 190
DB 181 KVKIKQDOTFKGMALAHVLEMSANPLDNGIEPBAFEV-TVPHIRIKALTSVPEKLP 239
QY 191 PSLTEHLIDGNKISRVDASIKGLNLAQGLSFNSISAVDNGSIANTPHLREHLDNKK 250
DB 240 PTLLEHLIDVYKISTVELEDFKRYKELQRLGLGNKKITDINGSLANIPIVREIHLNKK 299
QY 251 LTRVPGSLAEHKYIQVYVLLHNNNISVYSSDFPCPGHNTKRAVSQVSLFENPVQYMERIO 310
DB 300 LKKIPSGLEPKYQIILFHSNSIARVGVDNCFPTVPKKKSLYSALSIFNNPVKYMWO 359
QY 311 PSTFCVYVRSADQAGNY 328
DB 360 PATRCVLSRMSVQLGNP 377

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```

RESULT 22
US-09-944-944-2
Sequence 2, Application US/09944944
Patent No. US20020173463A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gertlisen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Auneeth
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,944
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092

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/ PRIOR FILING DATE: February 9, 1998
/ PRIOR APPLICATION NUMBER: 60/075,945
/ PRIOR FILING DATE: February 25, 1998
/ PRIOR APPLICATION NUMBER: 60/112,850
/ PRIOR FILING DATE: December 16, 1998
/ PRIOR APPLICATION NUMBER: 60/113,296
/ PRIOR FILING DATE: December 22, 1998
/ PRIOR APPLICATION NUMBER: 60/146,222
/ PRIOR FILING DATE: July 28, 1999
/ PRIOR APPLICATION NUMBER: PCT/US98/19330
/ PRIOR FILING DATE: September 16, 1998
/ PRIOR APPLICATION NUMBER: PCT/US98/25108
/ PRIOR FILING DATE: December 1, 1998
/ PRIOR APPLICATION NUMBER: 09/216,021
/ PRIOR FILING DATE: December 16, 1998
/ PRIOR APPLICATION NUMBER: 09/218,517
/ PRIOR FILING DATE: December 22, 1998
/ PRIOR APPLICATION NUMBER: 09/254,311
/ PRIOR FILING DATE: March 3, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/12252
/ PRIOR FILING DATE: June 22, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/21090
/ PRIOR FILING DATE: September 15, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/28409
/ PRIOR FILING DATE: No. US20020173463A member 30, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/28313
/ PRIOR FILING DATE: No. US20020173463A member 30, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/28301
/ PRIOR FILING DATE: December 1, 1999
/ PRIOR APPLICATION NUMBER: PCT/US99/30095
/ PRIOR FILING DATE: December 16, 1999
/ PRIOR APPLICATION NUMBER: PCT/US00/03565
/ PRIOR FILING DATE: February 11, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/04414
/ PRIOR FILING DATE: February 22, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/05841
/ PRIOR FILING DATE: March 2, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/08439
/ PRIOR FILING DATE: March 30, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/14042
/ PRIOR FILING DATE: May 22, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/20710
/ PRIOR FILING DATE: July 28, 2000
/ PRIOR APPLICATION NUMBER: PCT/US00/32678
/ PRIOR FILING DATE: December 1, 2000
/ PRIOR APPLICATION NUMBER: PCT/US01/06520
/ PRIOR FILING DATE: February 28, 2001
/ NUMBER OF SEQ ID NOS: 120
/ SEQ ID NO 2
/ LENGTH: 379
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-09-944-944-2

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Query Match 55.1%; Score 943.5; DB 10; Length 379;
Best Local Similarity 55.0%; Pred. No. 5.4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

11 PDDRDPEPSLGPVPCPCCHLRVVOCSDLGLDKVPDLPPTLLDLONNKITEIKDQ 70
61 PRSHFPPDLFPMPGCPGOCYSRVHCSDLGLTSVPTNIPFTRMDLONNKIKEIKEND 120
71 FKNLKNLHALLVNNKISKVSPGAFPLVKEERLYLSKNQKELPEKMPKTOELRAHEN 130
121 FKGLTSLYLGLILNNKLTKHHPKAFLLTKKLRRLYLSHNLSEIPLNLPKSLAEIRIHEN 180
131 EITKVRKVTNGLNOMIVIELGNPLKSSGIENGAFQGMKLSYIRIADTNITSTIQGLP 190
181 KVKKIQKQTFKGMNLAHVELEMSANPLDNNGIEPGAEGV-TVFHIRIAEAKLTSVPGKLP 239
191 PSTLEHLDNKISRVDASLKGILNMLAKGLSPFNSISAVDNGSLANTPHLREHLHDNNK 250
240 PTLLEHLHDYNNKISTVELEDFKRYKELQRLGLGNKKITIDENGSLANTPRVREIHLHNNK 299

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QY 251 LTRVPGSLAEHXYIQVYVLIHNNNISVVGSSDPCPPGHNTKASYSVSLFSNPOYWEIQ 310
DB 300 LKKIPSGLEIKLQIIFLHNSISIAVGVNDRCPTVPKAKKSLYSALISLNNPVKXWEMQ 359
QY 311 PSTFRCVVRSALIQAGNY 328
DB 360 PATFRCVLSRMSVQLGNF 377

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RESULT 23

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US-09-944-929-2
/ Sequence 2, Application US/0944929
/ Publication No. US20020197612A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin
/ APPLICANT: Botstein, David
/ APPLICANT: Baton, Dan
/ APPLICANT: Ferreira, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gerltsen, Mary
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul
/ APPLICANT: Grimaldi, Christopher
/ APPLICANT: Guiney, Austin
/ APPLICANT: Hillan, Kenneth
/ APPLICANT: Kijavlin, Ivar
/ APPLICANT: Napier, Mary
/ APPLICANT: Roy, Margaret
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Wood, William
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P2548P1C1
/ CURRENT APPLICATION NUMBER: US/09/944, 929
/ PRIOR FILING DATE: 2001-08-31
/ PRIOR APPLICATION NUMBER: 09/866, 028
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 120
/ SEQ ID NO 2
/ LENGTH: 379
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-09-944-929-2

```

```

Query Match 55.1%; Score 943.5; DB 10; Length 379;
Best Local Similarity 55.0%; Pred. No. 5.4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

```

```

QY 11 PDDRDPEPSLGPVPCPCCHLRVVOCSDLGLDKVPDLPPTLLDLONNKITEIKDQ 70
DB 61 PRSHFPPDLFPMPGCPGOCYSRVHCSDLGLTSVPTNIPFTRMDLONNKIKEIKEND 120
71 FKNLKNLHALLVNNKISKVSPGAFPLVKEERLYLSKNQKELPEKMPKTOELRAHEN 130
121 FKGLTSLYLGLILNNKLTKHHPKAFLLTKKLRRLYLSHNLSEIPLNLPKSLAEIRIHEN 180
131 EITKVRKVTNGLNOMIVIELGNPLKSSGIENGAFQGMKLSYIRIADTNITSTIQGLP 190
181 KVKKIQKQTFKGMNLAHVELEMSANPLDNNGIEPGAEGV-TVFHIRIAEAKLTSVPGKLP 239
191 PSTLEHLDNKISRVDASLKGILNMLAKGLSPFNSISAVDNGSLANTPHLREHLHDNNK 250
240 PTLLEHLHDYNNKISTVELEDFKRYKELQRLGLGNKKITIDENGSLANTPRVREIHLHNNK 299
QY 251 LTRVPGSLAEHXYIQVYVLIHNNNISVVGSSDPCPPGHNTKASYSVSLFSNPOYWEIQ 310
DB 300 LKKIPSGLEIKLQIIFLHNSISIAVGVNDRCPTVPKAKKSLYSALISLNNPVKXWEMQ 359
QY 311 PSTFRCVVRSALIQAGNY 328
DB 360 PATFRCVLSRMSVQLGNF 377

```

RESULT 24

US-09-944-907-2

; Sequence 2, Application US/09944907

; Publication No. US20020198147A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Batstein, David

; APPLICANT: Batson, Dan

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Hillan, Kenneth

; APPLICANT: Napier, Mary

; APPLICANT: Roy, Margaret

; APPLICANT: Tumas, Daniel

; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P2548P1C1

; CURRENT APPLICATION NUMBER: US/09/944,907

; PRIOR FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: 09/866,028

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 120

; SEQ ID NO 2

; LENGTH: 379

; TYPE: PRT

; ORGANISM: Homo Sapien

US-09-944-907-2

Query Match 55.1%; Score 943.5; DB 10; Length 379;

Best Local Similarity 55.0%; Pred. No. 5,4e-80;

Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

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QY 11 PDDRFBESLGPVCFRCQCHLRVQCSDLGDKVPKDLPPDTLLDLONNKITEIKGD 70
DB 61 PRSHFFPDLFPMCFPGQCSRVHCSDLGTSVPTIIPDTMLDLONNKIKEIKND 120
QY 71 FKNLKNLHALILVNNKISKVSPGAFPLVKERLYLSKNQKELPEKKPKTLOELRAHEN 130
DB 121 FKGLTSLYGLILNNKILTKHPKAFLLTKKRLRLYLSNQSLSEIPLNPKSLAEIRIHEN 180
QY 131 EITKRAKTYFNGLNQMIYIELGTNPLKSSGIENGAFQGMKKLSYRIADNTITSIPQGLP 190
DB 181 KYKKIQKDTFKGMNALHYLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLP 239
QY 191 PSTLEHLDGNKISRVDASIKGLNNLAKLGLSFNSISAVNGSLANTPHLEHLDNNK 250
DB 240 PTLLEHLDYNKISTVELEDFKRYKELQRLGLGNKKITDIENGSLANTPRVREHLENNK 299
QY 251 LTRVPGGLAEHKYIQVYLIHNNNISVVGSSDFPCPGHNTKASYSVGLFSNPVOYWEIQ 310
DB 300 LKKIPSGLPBELKYLIIFLHSNSIARVGVDPCFTVPKMKKSLYSALSLFNNPVAYWEIQ 359
QY 311 PSTRCVYVRSALIOLGNY 328
DB 360 PATFRCVLSRMSVQLGNF 377
```

RESULT 25

US-09-944-884-2

; Sequence 2, Application US/09944884

; Publication No. US20030077698A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Batstein, David

; APPLICANT: Batson, Dan

```
QY 11 PDDRFBESLGPVCFRCQCHLRVQCSDLGDKVPKDLPPDTLLDLONNKITEIKGD 70
DB 61 PRSHFFPDLFPMCFPGQCSRVHCSDLGTSVPTIIPDTMLDLONNKIKEIKND 120
QY 71 FKNLKNLHALILVNNKISKVSPGAFPLVKERLYLSKNQKELPEKKPKTLOELRAHEN 130
DB 121 FKGLTSLYGLILNNKILTKHPKAFLLTKKRLRLYLSNQSLSEIPLNPKSLAEIRIHEN 180
QY 131 EITKRAKTYFNGLNQMIYIELGTNPLKSSGIENGAFQGMKKLSYRIADNTITSIPQGLP 190
DB 181 KYKKIQKDTFKGMNALHYLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLP 239
QY 191 PSTLEHLDGNKISRVDASIKGLNNLAKLGLSFNSISAVNGSLANTPHLEHLDNNK 250
DB 240 PTLLEHLDYNKISTVELEDFKRYKELQRLGLGNKKITDIENGSLANTPRVREHLENNK 299
QY 251 LTRVPGGLAEHKYIQVYLIHNNNISVVGSSDFPCPGHNTKASYSVGLFSNPVOYWEIQ 310
DB 300 LKKIPSGLPBELKYLIIFLHSNSIARVGVDPCFTVPKMKKSLYSALSLFNNPVAYWEIQ 359
QY 311 PSTRCVYVRSALIOLGNY 328
DB 360 PATFRCVLSRMSVQLGNF 377
```

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Hillan, Kenneth

; APPLICANT: Kijavlin, Ivar

; APPLICANT: Napier, Mary

; APPLICANT: Roy, Margaret

; APPLICANT: Tumas, Daniel

; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P2548P1C1

; CURRENT APPLICATION NUMBER: US/09/944,884

; PRIOR FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: 09/866,028

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 120

; SEQ ID NO 2

; LENGTH: 379

; TYPE: PRT

; ORGANISM: Homo Sapien

US-09-944-884-2

Query Match 55.1%; Score 943.5; DB 11; Length 379;

Best Local Similarity 55.0%; Pred. No. 5,4e-80;

Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

```
QY 11 PDDRFBESLGPVCFRCQCHLRVQCSDLGDKVPKDLPPDTLLDLONNKITEIKGD 70
DB 61 PRSHFFPDLFPMCFPGQCSRVHCSDLGTSVPTIIPDTMLDLONNKIKEIKND 120
QY 71 FKNLKNLHALILVNNKISKVSPGAFPLVKERLYLSKNQKELPEKKPKTLOELRAHEN 130
DB 121 FKGLTSLYGLILNNKILTKHPKAFLLTKKRLRLYLSNQSLSEIPLNPKSLAEIRIHEN 180
QY 131 EITKRAKTYFNGLNQMIYIELGTNPLKSSGIENGAFQGMKKLSYRIADNTITSIPQGLP 190
DB 181 KYKKIQKDTFKGMNALHYLEMSANPLDNNGIEPGAFEGV-TVFHIRIAEAKLTSVPKGLP 239
QY 191 PSTLEHLDGNKISRVDASIKGLNNLAKLGLSFNSISAVNGSLANTPHLEHLDNNK 250
DB 240 PTLLEHLDYNKISTVELEDFKRYKELQRLGLGNKKITDIENGSLANTPRVREHLENNK 299
QY 251 LTRVPGGLAEHKYIQVYLIHNNNISVVGSSDFPCPGHNTKASYSVGLFSNPVOYWEIQ 310
DB 300 LKKIPSGLPBELKYLIIFLHSNSIARVGVDPCFTVPKMKKSLYSALSLFNNPVAYWEIQ 359
QY 311 PSTRCVYVRSALIOLGNY 328
DB 360 PATFRCVLSRMSVQLGNF 377
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RESULT 26

US-09-944-852-2

; Sequence 2, Application US/09944852

; Publication No. US20030083479A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Batstein, David

; APPLICANT: Batson, Dan

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Hillan, Kenneth

; APPLICANT: Kijavlin, Ivar

```

APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,852
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 2
LENGTH: 379
TYPE: PPT
ORGANISM: Homo Sapien
US-09-944-852-2

Query Match
Best Local Similarity 55.1%; Score 943.5; DB 11; Length 379;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDRFBSPLGVPCEFRCCCHLRVQCSDPLGLDKYKQDLPPTLLDQNNKITEIKOD 70
DB 61 PRSHFPFDLPFCMCFPGCCYGRVHCSDLGITSPVTNIPPTRMIDQNNKITEIKEND 120
QY 71 FRNLKMLHLLIVNNKISKVSFGATPLVKEKLYSKNQKLEPEKPKTLOELRAHEN 130
DB 121 FRGLSLVGLIANNKLTIKHPKAFLLTKQLRLYSHQSLSEIPLNPKSLAEIRIHEN 180
QY 131 EITVRKATVFNGLNOMIVELGTNPLKSGIENGAFQCKKLSYRIADNTITSIPQCLP 190
DB 181 KYKIKQKTFKCMALHYEWSANPLDNNGIEPGAEGV-TVFHRIAEAKLTSPKGLP 239
QY 191 PSTLEHLDGNKISVDAASLKLNNLAKLGISFNSISAVDNGSLANTPHLEHLDNNK 250
DB 240 PTLLEHLDYNNKISVLEDEDFRYKELQRLGKNNKIDIDENGSLANTPRAVEIHLENNK 299
QY 251 LTRVVGGLAEKHYITVYLIANNNISVVGSSDFCPGHNHTKASYSVGLFSNPVOYWEIQ 310
DB 300 LKKIPGSLPELKYLIQIIFLHSNSIARVGVNDPCFTVPKMKKSLYSALISLNNPVAYWEMQ 359
QY 311 PSTPCYVVRSAIOLGNY 328
DB 360 PATFRCVLSRMSVOLGNF 377

RESULT 27
US-09-943-780-2
Sequence 2, Application US/09943780
Publication No. US20030096742A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Batstein, David
APPLICANT: Baton, Dan
APPLICANT: Perrata, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gunney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/943,780
CURRENT FILING DATE: 2001-09-26

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PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,286
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20030096742A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20030096742A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678

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PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 2
LENGTH: 379
TYPE: PRT
ORGANISM: Homo Sapien
US-09-943-780-2

Query Match 55.1%; Score 943.5; DB 11; Length 379;
Best Local Similarity 55.0%; Pred. No. 5.4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDRDPFSLGVPVCFRCQCHLRVVOCSDDLGLDKVPKDLPPDTLLDLQNNKITEIKD 70
DB 61 PRSHFPFDLPFPMCPFGCCYSRVHCSDGLTSPVPTNIPDTRMLDLQNNKITEIKEND 120
QY 71 FKNLKNLHALILVNNKISKVSGAFPTPLVKLERLYLSKNQKELPEKMKPTLOELRAHEN 130
DB 121 FKGLTSLYGLILNNKLTIKHPKAFLTTKRLRLYLSHNSQSEIPLNPKSLAEIRHEN 180
QY 131 EITVRKRYTFNGLNQMTVIELGTNPLKSSGIENGAFOGMRKLSYIRADTNTISIPQGLP 190
DB 181 KVKKIQKDTFKGMALHVLMSANPLDNNNGIEPGAPEGV-TVPHIRIAEAKLTSPKGLP 239
QY 191 PSLTEHLHDGKISRVAASLKGANLAKLGLSFNSISAVNGSIANTPHLREHLDDNK 250
DB 240 PTLLEHLHDYKRISTVELEDFKRYKELQRLGLGNNKLTIDINGSLANIPRYREIHLDDNK 299
QY 251 LTRVPGSLAEHKYIQVYVYLNHNNSIVVSSDFCPGHNTKXASYSVGLFSPNPQYMEIQ 310
DB 300 LKKIPSGLEPKYLIQITFLHNSIARVGVNDFCPTVPKMKSLYSALSLFNNPVKYMEO 359
QY 311 PSTRCYVRSALQGNV 328
DB 360 PATRCVLSRMSVOLGNF 377

RESULT 28

US-10-137-870-328
Sequence 328, Application US/10137870
Publication No. US20030138683A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C15
CURRENT APPLICATION NUMBER: US/10/137,870
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 328
LENGTH: 379
TYPE: PRT
ORGANISM: Homo Sapien
US-10-137-870-328

Query Match 55.1%; Score 943.5; DB 12; Length 379;
Best Local Similarity 55.0%; Pred. No. 5.4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDRDPFSLGVPVCFRCQCHLRVVOCSDDLGLDKVPKDLPPDTLLDLQNNKITEIKD 70
DB 61 PRSHFPFDLPFPMCPFGCCYSRVHCSDGLTSPVPTNIPDTRMLDLQNNKITEIKEND 120
QY 71 FKNLKNLHALILVNNKISKVSGAFPTPLVKLERLYLSKNQKELPEKMKPTLOELRAHEN 130
DB 121 FKGLTSLYGLILNNKLTIKHPKAFLTTKRLRLYLSHNSQSEIPLNPKSLAEIRHEN 180
QY 131 EITVRKRYTFNGLNQMTVIELGTNPLKSSGIENGAFOGMRKLSYIRADTNTISIPQGLP 190
DB 181 KVKKIQKDTFKGMALHVLMSANPLDNNNGIEPGAPEGV-TVPHIRIAEAKLTSPKGLP 239
QY 191 PSLTEHLHDGKISRVAASLKGANLAKLGLSFNSISAVNGSIANTPHLREHLDDNK 250
DB 240 PTLLEHLHDYKRISTVELEDFKRYKELQRLGLGNNKLTIDINGSLANIPRYREIHLDDNK 299
QY 251 LTRVPGSLAEHKYIQVYVYLNHNNSIVVSSDFCPGHNTKXASYSVGLFSPNPQYMEIQ 310
DB 300 LKKIPSGLEPKYLIQITFLHNSIARVGVNDFCPTVPKMKSLYSALSLFNNPVKYMEO 359
QY 311 PSTRCYVRSALQGNV 328
DB 360 PATRCVLSRMSVOLGNF 377

RESULT 29

US-10-140-018-328
Sequence 328, Application US/10140018
Publication No. US20030138685A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C158
CURRENT APPLICATION NUMBER: US/10/140,018
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 328
LENGTH: 379
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-018-328

Query Match 55.1%; Score 943.5; DB 12; Length 379;
Best Local Similarity 55.0%; Pred. No. 5.4e-80;
Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDRDPFSLGVPVCFRCQCHLRVVOCSDDLGLDKVPKDLPPDTLLDLQNNKITEIKD 70
DB 61 PRSHFPFDLPFPMCPFGCCYSRVHCSDGLTSPVPTNIPDTRMLDLQNNKITEIKEND 120

QY 71 FKALKNLHALLVNNKISKVSPGAFPLVLYLERNKQKELPEKMPYTLQELRAHEN 130
 DB 121 FKGLTSLYGLILNNKKTJHPRKFLTYTKLRRLYSHNQLSEIPLNPKSLAELRIHEN 180
 QY 131 EITKRVKVTENGINOMIVIEIGTNPILKSGIENGAFQGMKKLSYIRIADNINISIPQGLP 190
 DB 181 KVKKIQDQTKGNMNLHVLEMSANPELDNNGIEPGEVGV-TVFHIRIAEAKLTSVPGKLP 239
 QY 191 PSTELHLDGNKISRVDASLKGILNLIKLGSLSNSISAVDNGSLANTPHLRELHLDNNK 250
 DB 240 PTLLEHLHDYNKISTVELDFPKRYKELQRLGLGNKKITDIENGSLANIPRVREHLHNNK 299
 QY 251 LTRVPGSLAEHKYIQVYVYLNHNNISVSGSDFCPPGHNTKASYSVGLFSNPVQWEIQ 310
 DB 300 LKKIPSGLEPKYLIQIIFLHNSNIARVGVNDFCPTVPKMKKSLYSALSIFNPNVKYWEQ 359
 QY 311 PSTFRVCYVRSALQGNV 328
 DB 360 PATFRCLSRMSVQLGNF 377

RESULT 30

US-10-140-021-328
 ; Sequence 328, Application US/10140021
 ; Publication No. US2003013886A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerltsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tuma, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3330R1C167
 ; CURRENT APPLICATION NUMBER: US/10/140,021
 ; CURRENT FILING DATE: 2002-05-06
 ; Prior Application removed - See Palm or File Wrapper
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 328
 ; LENGTH: 379
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-140-021-328

Query Match 55.1%; Score 943.5; DB 12; Length 379;
 Best Local Similarity 55.0%; Pred. No. 5.4e-80;
 Matches 175; Conservative 60; Mismatches 82; Indels 1; Gaps 1;

QY 11 PDDRDPEBGLGVCPPRCCHLRVOCSDLGDKVPKDLPPPTTLIDLNKKITETIKGD 70
 DB 61 PSHHPFPDLFPWCPGCGCYSRVHSCDGLTGVPTNIPPTRMIDLQNNKIKEIKEND 120
 QY 71 FKALKNLHALLVNNKISKVSPGAFPLVLYLERNKQKELPEKMPYTLQELRAHEN 130
 DB 121 FKGLTSLYGLILNNKKTJHPRKFLTYTKLRRLYSHNQLSEIPLNPKSLAELRIHEN 180
 QY 131 EITKRVKVTENGINOMIVIEIGTNPILKSGIENGAFQGMKKLSYIRIADNINISIPQGLP 190
 DB 181 KVKKIQDQTKGNMNLHVLEMSANPELDNNGIEPGEVGV-TVFHIRIAEAKLTSVPGKLP 239
 QY 191 PSTELHLDGNKISRVDASLKGILNLIKLGSLSNSISAVDNGSLANTPHLRELHLDNNK 250

DB 240 PTLLEHLHDYNKISTVELDFPKRYKELQRLGLGNKKITDIENGSLANIPRVREHLHNNK 299
 QY 251 LTRVPGSLAEHKYIQVYVYLNHNNISVSGSDFCPPGHNTKASYSVGLFSNPVQWEIQ 310
 DB 300 LKKIPSGLEPKYLIQIIFLHNSNIARVGVNDFCPTVPKMKKSLYSALSIFNPNVKYWEQ 359
 QY 311 PSTFRVCYVRSALQGNV 328
 DB 360 PATFRCLSRMSVQLGNF 377

Search completed: February 9, 2004, 11:48:19
 Job time : 81 secs